SEQUENCE LISTING

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ROOKEY, KRISTIN L.
HOET, RENE
HOOGENBOOM, HENDRICUS R. J. M.

<120> NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL LIBRARIES

<130> DYAX/002 CIP2

<140> 10/045,674
<141> 2001-10-25

<150> 06/198,069
<151> 2000-04-17

<150> 09/837,306
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<170> PatentIn Ver. 2.1

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<223> A, T, C or G

<220>
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<222> (87)
<223> A, T, C or G

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Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
1 5 10 15

wsn ttr mgn gcn gar gay acn gcn gtn tay tay tgy gcn aar 90
Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
20 25 30

<210> 91
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<220>
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FR3 protein sequence

<400> 91
Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
1 5 10 15

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
20 25 30

<210> 92
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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probe

<400> 92
agttctccct gcagctgaac tc 22

<210> 93
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<212> DNA
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<220>
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<400> 93
cactgtatct gcaaatgaac ag 22

<210> 94
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<220>
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<400> 94
ccctgtatct gcaaatgaac ag 22

<210> 95
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<210> 96
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cgctgtatct gcaaatgaac ag 22

<210> 97
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cggcatatct gcagatctgc ag 22

<210> 98
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cggcgtatct gcaaatgaac ag 22

<210> 99
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<400> 99
ctgcctacct gcagtggagc ag 22

<210> 100
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<220>
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tcgcctatct gcaaatgaac ag 22

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agg 63

<210> 102
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<220>
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<210> 103
<211> 54
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<210> 104
<211> 54
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<210> 105
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<400> 106
cgcttcacta agtctagaga c 21

<210> 107
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<220>
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<400> 107
acatggagct gagcagcctg ag 22

<210> 108
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<210> 110
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<210> 111
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<210> 112
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<220>
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<400> 112
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<210> 113
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<400> 113
atctgcaaat gaacagtctg ag 22

<210> 114
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<220>
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<400> 114
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<210> 115
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<220>
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<400> 115
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<210> 116
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<220>
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<400> 116
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<210> 117
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<220>
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<400> 117
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<210> 118
<211> 22
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<400> 118
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<210> 119
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<220>
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<400> 119
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<210> 120
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<220>
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<400> 120
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<210> 121
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<220>
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<400> 121
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<210> 122
<211> 22
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<220>
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<400> 122
ccctgaagct gagctctgtg ac 22

<210> 123
<211> 54
<212> DNA
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<220>
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<400> 123
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<210> 124
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<212> DNA
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<400> 124
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<210> 125
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<220>
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<220>
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<210> 128
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<220>
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<400> 128
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<210> 129
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ctgtgtatta ctgtgcgaga ga 22

<210> 130
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<400> 132
ccatgtatta ctgtgcaaga ta 22

<210> 133
<211> 22
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<400> 133
ccgtgtatta ctgtgcggca ga 22

<210> 134
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ccacatatta ctgtgcacac ag 22

<210> 135
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<400> 135
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<210> 136
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<400> 136
ccacgtatta ctgtgcacgg at 22

<210> 137
<211> 22
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<400> 137
ccttgtatta ctgtgcaaaa ga 22

<210> 138
<211> 22
<212> DNA
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<220>
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<400> 138
ctgtgtatta ctgtgcaaga ga 22

<210> 139
<211> 22
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<400> 139
ccgtgtatta ctgtaccaca ga 22

<210> 140
<211> 22
<212> DNA
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<400> 140
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<210> 141
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<400> 141
ccgtatatta ctgtgcgaaa ga 22

<210> 142
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<400> 142
ctgtgtatta ctgtgcgaaa ga 22

<210> 143
<211> 22
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ccgtgtatta ctgtactaga ga 22

<210> 144
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ccgtgtatta ctgtgctaga ga 22

<210> 145
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<210> 146
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<210> 147
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<210> 148
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<210> 149
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<400> 149
ctgtgtatta ctgtgcgaga ca 22

<210> 150
<211> 22
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<400> 150
ccatgtatta ctgtgcgaga ca 22

<210> 151
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<400> 151
ccatgtatta ctgtgcgaga 20

<210> 152
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<220>
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<400> 152
ccgtgtatta ctgtgcgaga g 21

<210> 153
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<400> 153
ctgtgtatta ctgtgcgaga g 21

<210> 154
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<400> 154
ccgtgtatta ctgtgcgaga g 21

<210> 155
<211> 21

<212> DNA
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<400> 155
ccgtatatta ctgtgcgaaa g 21

<210> 156
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<400> 156
ctgtgtatta ctgtgcgaaa g 21

<210> 157
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<212> DNA
<213> Artificial Sequence

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<400> 157
ctgtgtatta ctgtgcgaga c 21

<210> 158
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<400> 158
ccatgtatta ctgtgcgaga c 21

<210> 159
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 159
ccatgtatta ctgtgcgaga 20

<210> 160
<211> 94
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 160
ggtgtagtga tctagtgaca actctaagaa tactctctac ttgcagatga acagctttag 60
ggctgaggac actgcagtct actattgtgc gaga 94

<210> 161
<211> 94
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 161
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ggctgaggac actgcagtct actattgtgc gaaa 94

<210> 162
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 162
atagtagact gcagtgtcct cagcccttaa gctgttcatc tgcaagtaga gagtattctt 60
agagttgtct ctagatcact acacc 85

<210> 163
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 163
ggtgtagtga tctagagaca ac 22

<210> 164
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 164
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<210> 165
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 165
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<210> 166
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<213> Artificial Sequence

<220>
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<400> 166
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<210> 167
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<220>
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<400> 167
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<210> 168
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 168
ggtgtagtga aacagcttaa gggctg 26

<210> 169
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<220>
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<400> 169
agttctccct gcagctgaac tc 22

<210> 170
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<220>
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<400> 170
cactgtatct gcaaatgaac ag 22

<210> 171
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<400> 171
ccctgtatct gcaaatgaac ag 22

<210> 172
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<400> 172
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<210> 173
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<400> 173
cgctgtatct gcaaatgaac ag 22

<210> 174
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<400> 174
cggcatatct gcagatctgc ag 22

<210> 175
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<400> 175
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<210> 176
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<400> 176
ctgcctacct gcagtggagc ag 22

<210> 177
<211> 22

<212> DNA
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<220>
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<400> 177
tcgcctatct gcaaatgaac ag 22

<210> 178
<211> 22
<212> DNA
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<220>
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<400> 178
acatggagct gagcagcctg ag 22

<210> 179
<211> 22
<212> DNA
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 179
acatggagct gagcaggctg ag 22

<210> 180
<211> 22
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<220>
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<400> 180
acatggagct gaggagcctg ag 22

<210> 181
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<220>
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<400> 181
acctgcagtg gagcagcctg aa 22

<210> 182
<211> 22
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<220>
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<400> 182
atctgcaaat gaacagcctg aa 22

<210> 183
<211> 22
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<220>
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<400> 183
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<210> 184
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<400> 184
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<210> 185
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<400> 185
atctgcagat ctgcagccta aa 22

<210> 186
<211> 22
<212> DNA
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<220>
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<400> 186
atcttcaaat gaacagcctg ag 22

<210> 187
<211> 22
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<220>
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<400> 187
atcttcaaat gggcagcctg ag 22

<210> 188
<211> 22
<212> DNA
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<400> 188
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<210> 189
<211> 22
<212> DNA
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<400> 189
ccctgcagct gaactctgtg ac 22

<210> 190
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<400> 190
tccttacaat gaccaacatg ga 22

<210> 191
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<400> 191
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<210> 192
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<400> 192
ccgtgtatta ctgtgcgaga ga 22

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<400> 193
ctgtgtatta ctgtgcgaga ga 22

<210> 194
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<400> 194
ccgtgtatta ctgtgcgaga gg 22

<210> 195
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<400> 195
ccgtgtatta ctgtgcaaca ga 22

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<400> 196
ccatgtatta ctgtgcaaga ta 22

<210> 197
<211> 22
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<220>
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<400> 197
ccgtgtatta ctgtgcggca ga 22

<210> 198
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<400> 198
ccacatatta ctgtgcacac ag 22

<210> 199
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<400> 199
ccacatatta ctgtgcacgg at 22

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<210> 202
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ctgtgtatta ctgtgcaaga ga 22

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ccgtgtatta ctgtaccaca ga 22

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ccttgtatca ctgtgcgaga ga 22

<210> 205
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ctgtgtatta ctgtgcgaaa ga 22

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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 207
ccgtgtatta ctgtactaga ga 22

<210> 208
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 208
ccgtgtatta ctgtgctaga ga 22

<210> 209
<211> 22
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 209
ccgtgtatta ctgtactaga ca 22

<210> 210
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 210
ctgtgtatta ctgtaagaaa ga 22

<210> 211
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 211
ccgtgtatta ctgtgcgaga aa 22

<210> 212
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<212> DNA
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<220>
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<400> 212
ccgtgtatta ctgtgccaga ga 22

<210> 213
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 213
ctgtgtatta ctgtgcgaga ca 22

<210> 214
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 214
ccatgtatta ctgtgcgaga ca 22

<210> 215
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 215
ccatgtatta ctgtgcgaga aa 22

<210> 216
<211> 90
<212> DNA
<213> Homo sapiens

<400> 216
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tcctgcaagg cttctggata caccttcacc 90

<210> 217
<211> 90
<212> DNA
<213> Homo sapiens

<400> 217
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tcctgcaagg cttctggata caccttcact 90

<210> 218
<211> 90
<212> DNA
<213> Homo sapiens

<400> 218
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tcctgcaagg cttctggata caccttcacc 90

<210> 219
<211> 90
<212> DNA
<213> Homo sapiens

<400> 219
caggttcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggtta cacctttacc 90

<210> 220
<211> 90
<212> DNA
<213> Homo sapiens

<400> 220
caggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg tttccggata caccctcact 90

<210> 221
<211> 90
<212> DNA
<213> Homo sapiens

<400> 221
cagatgcagc tggtgcagtc tggggctgag gtgaagaaga ctgggtcctc agtgaaggtt 60
tcctgcaagg cttccggata caccttcacc 90

<210> 222
<211> 90
<212> DNA
<213> Homo sapiens

<400> 222
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60
tcctgcaagg catctggata caccttcacc 90

<210> 223
<211> 90

<212> DNA
<213> Homo sapiens

<400> 223
caaatgcagc tggtgcagtc tgggcctgag gtgaagaagc ctgggacctc agtgaaggtc 60
tcctgcaagg cttctggatt cacctttact 90

<210> 224
<211> 90
<212> DNA
<213> Homo sapiens

<400> 224
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60
tcctgcaagg cttctggagg caccttcagc 90

<210> 225
<211> 90
<212> DNA
<213> Homo sapiens

<400> 225
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tcctgcaagg cttctggagg caccttcagc 90

<210> 226
<211> 90
<212> DNA
<213> Homo sapiens

<400> 226
gaggtccagc tggtacagtc tggggctgag gtgaagaagc ctggggctac agtgaaaatc 60
tcctgcaagg tttctggata caccttcacc 90

<210> 227
<211> 90
<212> DNA
<213> Homo sapiens

<400> 227
cagatcacct tgaaggagtc tggtcctacg ctggtgaaac ccacacagac cctcacgctg 60
acctgcacct tctctgggtt ctcactcagc 90

<210> 228
<211> 90
<212> DNA
<213> Homo sapiens

<400> 228
caggtcacct tgaaggagtc tggtcctgtg ctggtgaaac ccacagagac cctcacgctg 60
acctgcaccg tctctgggtt ctcactcagc 90

<210> 229
<211> 90
<212> DNA
<213> Homo sapiens

<400> 229
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acctgcacct tctctgggtt ctcactcagc 90

<210> 230
<211> 90
<212> DNA
<213> Homo sapiens

<400> 230
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tcctgtgcag cctctggatt cacctttagt 90

<210> 231
<211> 90
<212> DNA
<213> Homo sapiens

<400> 231
gaagtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat 90

<210> 232
<211> 90
<212> DNA
<213> Homo sapiens

<400> 232
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tcctgtgcag cctctggatt caccttcagt 90

<210> 233
<211> 90
<212> DNA
<213> Homo sapiens

<400> 233
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tcctgtgcag cctctggatt caccttcagt 90

<210> 234
<211> 90
<212> DNA
<213> Homo sapiens

<400> 234
gaggtgcagc tggtggagtc tgggggaggc ttggtaaagc ctgggggggtc ccttagactc 60
tcctgtgcag cctctggatt cactttcagt 90

<210> 235
<211> 90
<212> DNA
<213> Homo sapiens

<400> 235
gaggtgcagc tggtggagtc tgggggaggt gtggtacggc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat 90

<210> 236
<211> 90
<212> DNA
<213> Homo sapiens

<400> 236
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tcctgtgcag cctctggatt caccttcagt 90

<210> 237
<211> 90
<212> DNA
<213> Homo sapiens

<400> 237
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tcctgtgcag cctctggatt cacctttagc 90

<210> 238
<211> 90
<212> DNA
<213> Homo sapiens

<400> 238
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt 90

<210> 239
<211> 90
<212> DNA
<213> Homo sapiens

<400> 239
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt 90

<210> 240
<211> 90
<212> DNA
<213> Homo sapiens

<400> 240
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt 90

<210> 241
<211> 90
<212> DNA
<213> Homo sapiens

<400> 241
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt 90

<210> 242
<211> 90
<212> DNA
<213> Homo sapiens

<400> 242
gaagtgcagc tggtggagtc tgggggagtc gtggtacagc ctgggggGtc cctgagactc 60
tcctgtgcag cctctggatt caccTttgat 90

<210> 243
<211> 90
<212> DNA
<213> Homo sapiens

<400> 243
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggGtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt 90

<210> 244
<211> 90
<212> DNA
<213> Homo sapiens

<400> 244
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cagggcggtc cctgagactc 60
tcctgtacag cttctggatt caccTttggt 90

<210> 245
<211> 90
<212> DNA
<213> Homo sapiens

<400> 245
gaggtgcagc tggtggagac tggaggaggc ttgatccagc ctgggggGtc cctgagactc 60
tcctgtgcag cctctgggtt caccgtcagt 90

<210> 246
<211> 90
<212> DNA

<213> Homo sapiens

<400> 246
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt 90

<210> 247
<211> 90
<212> DNA
<213> Homo sapiens

<400> 247
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt caccgtcagt 90

<210> 248
<211> 90
<212> DNA
<213> Homo sapiens

<400> 248
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctggagggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt 90

<210> 249
<211> 90
<212> DNA
<213> Homo sapiens

<400> 249
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctgaaactc 60
tcctgtgcag cctctgggtt caccttcagt 90

<210> 250
<211> 90
<212> DNA
<213> Homo sapiens

<400> 250
gaggtgcagc tggtggagtc cgggggaggc ttagttcagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt caccttcagt 90

<210> 251
<211> 90
<212> DNA
<213> Homo sapiens

<400> 251
gaggtgcagc tggtggagtc tcggggagtc ttggtacagc ctgggggtc cctgagactc 60
tcctgtgcag cctctggatt caccgtcagt 90

<210> 252
<211> 90
<212> DNA
<213> Homo sapiens

<400> 252
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggggac cctgtccctc 60
acctgcgctg tctctggtgg ctccatcagc 90

<210> 253
<211> 90
<212> DNA
<213> Homo sapiens

<400> 253
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggacac cctgtccctc 60
acctgcgctg tctctggtta ctccatcagc 90

<210> 254
<211> 90
<212> DNA
<213> Homo sapiens

<400> 254
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc 90

<210> 255
<211> 90
<212> DNA
<213> Homo sapiens

<400> 255
cagctgcagc tgcaggagtc cggctcagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcgctg tctctggtgg ctccatcagc 90

<210> 256
<211> 90
<212> DNA
<213> Homo sapiens

<400> 256
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc 90

<210> 257
<211> 90
<212> DNA
<213> Homo sapiens

<400> 257
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcacagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc 90

<210> 258
<211> 90
<212> DNA
<213> Homo sapiens

<400> 258
caggtgcagc tacagcagtg gggcgcagga ctgttgaagc cttcggagac cctgtccctc 60
acctgcgctg tctatggtgg gtccttcagt 90

<210> 259
<211> 90
<212> DNA
<213> Homo sapiens

<400> 259
cagctgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccatcagc 90

<210> 260
<211> 90
<212> DNA
<213> Homo sapiens

<400> 260
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acctgcactg tctctggtgg ctccatcagt 90

<210> 261
<211> 90
<212> DNA
<213> Homo sapiens

<400> 261
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcactg tctctggtgg ctccgtcagc 90

<210> 262
<211> 90
<212> DNA
<213> Homo sapiens

<400> 262
caggtgcagc tgcaggagtc gggcccagga ctggtgaagc cttcggagac cctgtccctc 60
acctgcgctg tctctggtta ctccatcagc 90

<210> 263
<211> 90
<212> DNA
<213> Homo sapiens

<400> 263
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60
tcctgtaagg gttctggata cagctttacc 90

<210> 264
<211> 90
<212> DNA
<213> Homo sapiens

<400> 264
gaagtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaggatc 60
tcctgtaagg gttctggata cagctttacc 90

<210> 265
<211> 90
<212> DNA
<213> Homo sapiens

<400> 265
caggtacagc tgcagcagtc aggtccagga ctggtgaagc cctcgcagac cctctcactc 60
acctgtgcca tctccgggga cagtgtctct 90

<210> 266
<211> 90
<212> DNA
<213> Homo sapiens

<400> 266
caggtgcagc tggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60
tcctgcaagg cttctggata caccttcact 90

<210> 267
<211> 22
<212> DNA
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<220>
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oligonucleotide

<400> 267
ccgtgtatta ctgtgcgaga ga 22

<210> 268
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 268
ctgtgtatta ctgtgcgaga ga 22

<210> 269
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 269
ccgtgtatta ctgtgcgaga gg 22

<210> 270
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 270
ccgtatatta ctgtgcgaaa ga 22

<210> 271
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 271
ctgtgtatta ctgtgcgaaa ga 22

<210> 272
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 272
ctgtgtatta ctgtgcgaga ca 22

<210> 273
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 273
ccatgtatta ctgtgcgaga ca 22

<210> 274
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 274
ccatgtatta ctgtgcgaga aa 22

<210> 275
<211> 69
<212> DNA
<213> Homo sapiens

<400> 275
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 276
<211> 69
<212> DNA
<213> Homo sapiens

<400> 276
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 277
<211> 69
<212> DNA
<213> Homo sapiens

<400> 277
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 278
<211> 69
<212> DNA
<213> Homo sapiens

<400> 278
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 279
<211> 69
<212> DNA
<213> Homo sapiens

<400> 279
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 280
<211> 69
<212> DNA
<213> Homo sapiens

<400> 280
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 281
<211> 69
<212> DNA
<213> Homo sapiens

<400> 281
aacatccaga tgacccagtc tccatctgcc atgtctgcat ctgtaggaga cagagtcacc 60
atcacttgt 69

<210> 282
<211> 69
<212> DNA
<213> Homo sapiens

<400> 282
gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgt 69

<210> 283
<211> 69
<212> DNA
<213> Homo sapiens

<400> 283
gacatccaga tgacccagtc tccatcctca ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgt 69

<210> 284
<211> 69

<212> DNA
<213> Homo sapiens

<400> 284
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atcacttgc 69

<210> 285
<211> 69
<212> DNA
<213> Homo sapiens

<400> 285
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 286
<211> 69
<212> DNA
<213> Homo sapiens

<400> 286
gacatccaga tgacccagtc tccatcttcc gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgt 69

<210> 287
<211> 69
<212> DNA
<213> Homo sapiens

<400> 287
gacatccaga tgacccagtc tccatcttct gtgtctgcat ctgtaggaga cagagtcacc 60
atcacttgt 69

<210> 288
<211> 69
<212> DNA
<213> Homo sapiens

<400> 288
gacatccagt tgacccagtc tccatccttc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 289
<211> 69
<212> DNA
<213> Homo sapiens

<400> 289
gccatccgga tgacccagtc tccattctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 290
<211> 69
<212> DNA
<213> Homo sapiens

<400> 290
gccatccgga tgacccagtc tccatcctca ttctctgcat ctacaggaga cagagtcacc 60
atcacttgt 69

<210> 291
<211> 69
<212> DNA
<213> Homo sapiens

<400> 291
gtcatctgga tgacccagtc tccatcctta ctctctgcat ctacaggaga cagagtcacc 60
atcagttgt 69

<210> 292
<211> 69
<212> DNA
<213> Homo sapiens

<400> 292
gccatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 293
<211> 69
<212> DNA
<213> Homo sapiens

<400> 293
gacatccaga tgacccagtc tccttccacc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgc 69

<210> 294
<211> 69
<212> DNA
<213> Homo sapiens

<400> 294
gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgc 69

<210> 295
<211> 69
<212> DNA
<213> Homo sapiens

<400> 295
gatattgtga tgacccagac tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgc 69

<210> 296
<211> 69
<212> DNA
<213> Homo sapiens

<400> 296
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60
atctcctgc 69

<210> 297
<211> 69
<212> DNA
<213> Homo sapiens

<400> 297
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60
atctcctgc 69

<210> 298
<211> 69
<212> DNA
<213> Homo sapiens

<400> 298
gatattgtga tgacccagac tccactctct ctgtccgtca cccctggaca gccggcctcc 60
atctcctgc 69

<210> 299
<211> 69
<212> DNA
<213> Homo sapiens

<400> 299
gatattgtga tgacccagac tccactctct ctgtccgtca cccctggaca gccggcctcc 60
atctcctgc 69

<210> 300
<211> 69
<212> DNA
<213> Homo sapiens

<400> 300
gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgc 69

<210> 301
<211> 69
<212> DNA
<213> Homo sapiens

<400> 301
gatattgtga tgactcagtc tccactctcc ctgcccgtca cccctggaga gccggcctcc 60
atctcctgc 69

<210> 302
<211> 69
<212> DNA
<213> Homo sapiens

<400> 302
gatattgtga tgacccagac tccactctcc tcacctgtca cccttggaca gccggcctcc 60
atctcctgc 69

<210> 303
<211> 69
<212> DNA
<213> Homo sapiens

<400> 303
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgc 69

<210> 304
<211> 69
<212> DNA
<213> Homo sapiens

<400> 304
gaaattgtgt tgacgcagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgc 69

<210> 305
<211> 69
<212> DNA
<213> Homo sapiens

<400> 305
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
ctctcctgc 69

<210> 306
<211> 69
<212> DNA
<213> Homo sapiens

<400> 306
gaaatagtga tgacgcagtc tccagccacc ctgtctgtgt ctccagggga aagagccacc 60
ctctcctgc 69

<210> 307
<211> 69

<212> DNA
<213> Homo sapiens

<400> 307
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgc 69

<210> 308
<211> 69
<212> DNA
<213> Homo sapiens

<400> 308
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgc 69

<210> 309
<211> 69
<212> DNA
<213> Homo sapiens

<400> 309
gaaattgtaa tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60
ctctcctgc 69

<210> 310
<211> 69
<212> DNA
<213> Homo sapiens

<400> 310
gacatcgtga tgacccagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60
atcaactgc 69

<210> 311
<211> 69
<212> DNA
<213> Homo sapiens

<400> 311
gaaacgacac tcacgcagtc tccagcattc atgtcagcga ctccaggaga caaagtcaac 60
atctcctgc 69

<210> 312
<211> 69
<212> DNA
<213> Homo sapiens

<400> 312
gaaattgtgc tgactcagtc tccagacttt cagtctgtga ctccaaagga gaaagtcacc 60
atcacctgc 69

<210> 313
<211> 69
<212> DNA
<213> Homo sapiens

<400> 313
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atcacctgc 69

<210> 314
<211> 69
<212> DNA
<213> Homo sapiens

<400> 314
gatgttgtga tgacacagtc tccagctttc ctctctgtga ctccagggga gaaagtcacc 60
atcacctgc 69

<210> 315
<211> 66
<212> DNA
<213> Homo sapiens

<400> 315
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tcctgt 66

<210> 316
<211> 66
<212> DNA
<213> Homo sapiens

<400> 316
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tcctgc 66

<210> 317
<211> 66
<212> DNA
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<400> 317
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tcttgt 66

<210> 318
<211> 66
<212> DNA
<213> Homo sapiens

<400> 318
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tcttgt 66

<210> 319
<211> 66
<212> DNA
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<400> 319
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tcctgc 66

<210> 320
<211> 66
<212> DNA
<213> Homo sapiens

<400> 320
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tcctgc 66

<210> 321
<211> 66
<212> DNA
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tcctgc 66

<210> 322
<211> 66
<212> DNA
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<400> 322
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tcctgc 66

<210> 323
<211> 66
<212> DNA
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<400> 323
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tcctgc 66

<210> 324
<211> 66
<212> DNA
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<400> 324

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tcctgc 66

<210> 325
<211> 66
<212> DNA
<213> Homo sapiens

<400> 325
tcctatgagc tgactcagcc accctcagtg tccgtgtccc caggacagac agccagcatc 60
acctgc 66

<210> 326
<211> 66
<212> DNA
<213> Homo sapiens

<400> 326
tcctatgagc tgactcagcc actctcagtg tcagtggccc tgggacagac ggccaggatt 60
acctgt 66

<210> 327
<211> 66
<212> DNA
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<400> 327
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acctgc 66

<210> 328
<211> 66
<212> DNA
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<400> 328
tcctatgagc tgacacagcc accctcggtg tcagtgtccc taggacagat ggccaggatc 60
acctgc 66

<210> 329
<211> 66
<212> DNA
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<400> 329
tcttctgagc tgactcagga ccctgctgtg tctgtggcct tgggacagac agtcaggatc 60
acatgc 66

<210> 330
<211> 66
<212> DNA
<213> Homo sapiens

<400> 330
tcctatgtgc tgactcagcc accctcagtg tcagtggccc caggaaagac ggccaggatt 60
acctgt 66

<210> 331
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<400> 331
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acctgc 66

<210> 332
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acctgc 66

<210> 333
<211> 66
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<400> 333
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acctgc 66

<210> 334
<211> 66
<212> DNA
<213> Homo sapiens

<400> 334
ctgcctgtgc tgactcagcc cccgtctgca tctgccttgc tgggagcctc gatcaagctc 60
acctgc 66

<210> 335
<211> 66
<212> DNA
<213> Homo sapiens

<400> 335
cagcctgtgc tgactcaatc atcctctgcc tctgcttccc tgggatcctc ggtcaagctc 60
acctgc 66

<210> 336
<211> 66

<212> DNA
<213> Homo sapiens

<400> 336
cagcttgtgc tgactcaatc gccctctgcc tctgcctccc tgggagcctc ggtcaagctc 60
acctgc 66

<210> 337
<211> 66
<212> DNA
<213> Homo sapiens

<400> 337
cagcctgtgc tgactcagcc accttcctcc tccgcatctc ctggagaatc cgccagactc 60
acctgc 66

<210> 338
<211> 66
<212> DNA
<213> Homo sapiens

<400> 338
caggctgtgc tgactcagcc ggcttccctc tctgcatctc ctggagcatc agccagtctc 60
acctgc 66

<210> 339
<211> 66
<212> DNA
<213> Homo sapiens

<400> 339
cagcctgtgc tgactcagcc atcttcccat tctgcatctt ctggagcatc agtcagactc 60
acctgc 66

<210> 340
<211> 66
<212> DNA
<213> Homo sapiens

<400> 340
aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc 60
tcctgc 66

<210> 341
<211> 66
<212> DNA
<213> Homo sapiens

<400> 341
cagactgtgg tgactcagga gccctcactg actgtgtccc caggagggac agtcactctc 60
acctgt 66

<210> 342
<211> 66
<212> DNA
<213> Homo sapiens

<400> 342
caggctgtgg tgactcagga gccctcactg actgtgtccc caggagggac agtcactctc 60
acctgt 66

<210> 343
<211> 66
<212> DNA
<213> Homo sapiens

<400> 343
cagactgtgg tgacccagga gccatcgttc tcagtgtccc ctggagggac agtcacactc 60
acttgt 66

<210> 344
<211> 66
<212> DNA
<213> Homo sapiens

<400> 344
cagcctgtgc tgactcagcc accttctgca tcagcctccc tgggagcctc ggtcacactc 60
acctgc 66

<210> 345
<211> 66
<212> DNA
<213> Homo sapiens

<400> 345
caggcagggc tgactcagcc accctcggtg tccaagggct tgagacagac cgccacactc 60
acctgc 66

<210> 346
<211> 11
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<220>
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oligonucleotide

<220>
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<222> (1)..(6)
<223> A, T, C, G, other or unknown

<400> 346
nnnnnngact c 11

<210> 347
<211> 11
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<223> A, T, C, G, other or unknown

<400> 347
gagtcnnnnn n 11

<210> 348
<211> 11
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<222> (3)..(9)
<223> A, T, C, G, other or unknown

<400> 348
gcnnnnnnng c 11

<210> 349
<211> 11
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(11)
<223> A, T, C, G, other or unknown

<400> 349
acctgcnnnn n 11

<210> 350
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 350
cacatccgtg ttgttcacgg atgtg 25

<210> 351
<211> 88
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 351
aatagtagac tgcagtgtcc tcagccctta agctgttcat ctgcaagtag agagtattct 60
tagagttgtc tctagactta gtgaagcg 88

<210> 352
<211> 88
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 352
cgcttcacta agtctagaga caactctaag aatactctct acttgcagat gaacagctta 60
agggctgagg acactgcagt ctactatt 88

<210> 353
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 353
cgcttcacta agtctagaga caactctaag aatactctct acttgcagat gaacagctta 60
agggctgagg acactgcagt ctactattgt gcgag 95

<210> 354
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 354
cgcttcacta agtctagaga caactctaag aatactctct acttgcagat gaacagctta 60
agggctgagg acactgcagt ctactattgt acgag 95

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 355
cgcttcacta agtctagaga caac 24

<210> 356
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (8)..(15)
<223> A, T, C, G, other or unknown

<400> 356
cacctgcnnn nnnnn 15

<210> 357
<211> 17
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<222> (7)..(17)
<223> A, T, C, G, other or unknown

<400> 357
cagctcnnnn nnnnnnn 17

<210> 358
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<212> DNA
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<220>
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<220>
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<223> A, T, C, G, other or unknown

<400> 358
gaagacnnnn nnnnnnn 17

<210> 359
<211> 17
<212> DNA
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<220>
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<220>
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<223> A, T, C, G, other or unknown

<400> 359
gcagcnnnnn nnnnnnn 17

<210> 360
<211> 12
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<220>
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<220>
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<223> A, T, C, G, other or unknown

<400> 360
gaagacnnnn nn 12

<210> 361
<211> 22
<212> DNA
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<220>
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<220>
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<223> A, T, C, G, other or unknown

<400> 361
cttgagnnnn nnnnnnnnnn nn 22

<210> 362
<211> 19
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(19)
<223> A, T, C, G, other or unknown

<400> 362
acggcnnnnn nnnnnnnnn 19

<210> 363
<211> 18
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(18)
<223> A, T, C, G, other or unknown

<400> 363
acggcnnnnn nnnnnnnn 18

<210> 364
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(12)
<223> A, T, C, G, other or unknown

<400> 364
gtatccnnnn nn 12

<210> 365
<211> 11
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(11)
<223> A, T, C, G, other or unknown

<400> 365
actgggnnnn n 11

<210> 366
<211> 10
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(10)
<223> A, T, C, G, other or unknown

<400> 366
ggatcnnnnn 10

<210> 367
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(11)

<223> A, T, C, G, other or unknown

<400> 367
gcatcnnnnn n 11

<210> 368
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(16)
<223> A, T, C, G, other or unknown

<400> 368
gaggagnnnn nnnnnn 16

<210> 369
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(19)
<223> A, T, C, G, other or unknown

<400> 369
gggacnnnnn nnnnnnnnn 19

<210> 370
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(14)
<223> A, T, C, G, other or unknown

<400> 370
acctgcnnnn nnnn 14

<210> 371
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(17)
<223> A, T, C, G, other or unknown

<400> 371
ggcggannnn nnnnnnn 17

<210> 372
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(22)
<223> A, T, C, G, other or unknown

<400> 372
ctgaagnnnn nnnnnnnnnn nn 22

<210> 373
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(11)
<223> A, T, C, G, other or unknown

<400> 373
cccgcnnnnn n 11

<210> 374
<211> 18

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(18)
<223> A, T, C, G, other or unknown

<400> 374
ggatgnnnnn nnnnnnnn 18

<210> 375
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<222> (7)..(22)
<223> A, T, C, G, other or unknown

<400> 375
ctggagnnnn nnnnnnnnnn nn 22

<210> 376
<211> 15
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(15)
<223> A, T, C, G, other or unknown

<400> 376
gacgcnnnnn nnnnn 15

<210> 377
<211> 13
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(13)
<223> A, T, C, G, other or unknown

<400> 377
ggtgannnnn nnn 13

<210> 378
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(13)
<223> A, T, C, G, other or unknown

<400> 378
gaagannnnn nnn 13

<210> 379
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(10)
<223> A, T, C, G, other or unknown

<400> 379
gagtcnnnnn 10

<210> 380
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<222> (7)..(26)
<223> A, T, C, G, other or unknown

<400> 380
tccracnnnn nnnnnnnnnn nnnnnn 26

<210> 381
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (5)..(11)
<223> A, T, C, G, other or unknown

<400> 381
cctcnnnnnn n 11

<210> 382
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(10)
<223> A, T, C, G, other or unknown

<400> 382
gagtcnnnnn 10

<210> 383
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(18)
<223> A, T, C, G, other or unknown

<400> 383
cccacannnn nnnnnnnn 18

<210> 384
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(14)
<223> A, T, C, G, other or unknown

<400> 384
gcatcnnnnn nnnn 14

<210> 385
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(13)
<223> A, T, C, G, other or unknown

<400> 385
ggtgannnnn nnn 13

<210> 386
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (5)..(12)
<223> A, T, C, G, other or unknown

<400> 386
cccgnnnnnn nn 12

<210> 387
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (6)..(19)
<223> A, T, C, G, other or unknown

<400> 387
ggatgnnnnn nnnnnnnnn 19

<210> 388
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(17)
<223> A, T, C, G, other or unknown

<400> 388
gaccgannnn nnnnnnn 17

<210> 389
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(17)
<223> A, T, C, G, other or unknown

<400> 389
cacccannnn nnnnnnn 17

<210> 390
<211> 17
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(17)
<223> A, T, C, G, other or unknown

<400> 390
caarcannnn nnnnnnn 17

<210> 391
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic probe

<400> 391
gctgtgtatt actgtgcgag 20

<210> 392
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic probe

<400> 392
gccgtgtatt actgtgcgag 20

<210> 393
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic probe

<400> 393
gccgtatatt actgtgcgag 20

<210> 394
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic probe

<400> 394
gccgtgtatt actgtacgag 20

<210> 395
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic probe

<400> 395
gccatgtatt actgtgcgag 20

<210> 396
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 396
cacatccgtg ttgttcacgg atgtg 25

<210> 397
<211> 88
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 397
aatagtagac tgcagtgtcc tcagccctta agctgttcat ctgcaagtag agagtattct 60
tagagttgtc tctagactta gtgaagcg 88

<210> 398
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 398
cgcttcacta agtctagaga caactctaag aatactctct acttgcagat gaacagctta 60
agggctgagg acactgcagt ctactattgt gcgag 95

<210> 399
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 399
cgcttcacta agtctagaga caac 24

<210> 400
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 400
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<210> 401
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 401
cacatccgtg ttgttcacgg atgtgggaga gtggagactg agtc 44

<210> 402
<211> 44
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 402
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<210> 403

<211> 44
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 403
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<210> 404
<211> 34
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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cctctactct tgtcacagtg cacaagacat ccag 34

<210> 405
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 405
cctctactct tgtcacagtg 20

<210> 406
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 406
ggaggatgga ctggatgtct tgtgcactgt gacaagagta gagg 44

<210> 407
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 407
ggagagtgga ctggatgtct tgtgcactgt gacaagagta gagg 44

<210> 408
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 408
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<210> 409
<211> 44
<212> DNA
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<220>
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<400> 409
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<210> 410
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<220>
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<210> 411
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<220>
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<400> 411
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<210> 412
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<220>
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<400> 412
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<210> 413
<211> 44
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 413
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<210> 414
<211> 59
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<210> 415
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<212> DNA
<213> Artificial Sequence

<220>
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acagtcgat 69

<210> 416
<211> 69
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<220>
<223> Description of Artificial Sequence: Synthetic
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acagacagt 69

<210> 417
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

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acagtcagt 69

<210> 418
<211> 70
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 418
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ggcagagggt 70

<210> 419
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 419
cctctgactg agtgcacaga gtgc 24

<210> 420
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<220>
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<223> A, T, C, G, other or unknown

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<210> 421
<211> 15
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<223> A, T, C, G, other or unknown

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<210> 422
<211> 12
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<220>
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<210> 423
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
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<223> A, T, C, G, other or unknown

<400> 423
gccnnnnngg c 11

<210> 424
<211> 10
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<223> A, T, C, G, other or unknown

<400> 424
gatnnnnatc 10

<210> 425
<211> 11
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<223> A, T, C, G, other or unknown

<400> 425
gacnnnnngt c 11

<210> 426
<211> 11
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<223> A, T, C, G, other or unknown

<400> 426
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<210> 427
<211> 12
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<223> A, T, C, G, other or unknown

<400> 427
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<210> 428
<211> 12
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<220>
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<220>
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<223> A, T, C, G, other or unknown

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gacnnnnnng tc 12

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<223> A, T, C, G, other or unknown

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ccannnnntg g 11

<210> 430
<211> 12

<212> DNA
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<220>
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<220>
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<223> A, T, C, G, other or unknown

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nnnnnngaga cg 12

<210> 431
<211> 12
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<220>
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<210> 432
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<223> A, T, C, G, other or unknown

<400> 434
nnnnnnnnnn ctcctc 16

<210> 435
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<223> A, T, C, G, other or unknown

<400> 435
nnnnnnnnnt ccgcc 15

<210> 436
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<221> modified_base
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<223> A, T, C, G, other or unknown

<400> 436
ggccnnnnng gcc 13

<210> 437
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<400> 438
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<210> 440
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<210> 441
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<210> 443
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<400> 444
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ggtctcnnnn n 11

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<220>
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<223> A, T, C, G, other or unknown

<400> 447
gccnnnnngg c 11

<210> 448
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<220>
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<223> A, T, C, G, other or unknown

<400> 448
ccannnnnnn nntgg 15

<210> 449
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<223> A, T, C, G, other or unknown

<400> 449
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<210> 450
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<223> A, T, C, G, other or unknown

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<400> 451

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cgttcgcaga attgggaatc aactgttaca tggaatgaaa cttccagaca ccgtacttta 180

gttgcatatt taaaacatgt tgagctacag caccagattc agcaattaag ctctaagcca 240

tccgcaaaaa tgacctctta tcaaaaggag caattaaagg tactctctaa tcctgacctg 300

ttggagtttg cttccggtct ggttcgcttt gaagctcgaa ttaaaacgcg atatttgaag 360

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                Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val
                  1               5                  10

gtt cct ttc tat tct cac agt gca cag tctgtcgtga cgcagccgcc         1658
Val Pro Phe Tyr Ser His Ser Ala Gln
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          15                  20

ctcagtgtct ggggccccag ggcagagggt caccatctcc tgcactggga gcagctccaa 1718

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cctcatctat ggtaacagca atcggccctc aggggtccct gaccgattct ctggctccaa 1838

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                          Met Lys Tyr Leu Leu Pro Thr Ala Ala
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gct gga ttg tta tta ctc gcg gcc cag ccg gcc atg gcc gaa gtt caa    2417
Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met Ala Glu Val Gln
 30                  35                  40                  45

ttg tta gag tct ggt ggc ggt ctt gtt cag cct ggt ggt tct tta cgt    2465
Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
                 50                  55                  60

ctt tct tgc gct gct tcc gga ttc act ttc tct tcg tac gct atg tct    2513
Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
             65                  70                  75

tgg gtt cgc caa gct cct ggt aaa ggt ttg gag tgg gtt tct gct atc    2561
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile
         80                  85                  90

tct ggt tct ggt ggc agt act tac tat gct gac tcc gtt aaa ggt cgc    2609
Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
     95                 100                 105

ttc act atc tct aga gac aac tct aag aat act ctc tac ttg cag atg    2657
Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
110                 115                 120                 125

aac agc tta agg gct gag gac act gca gtc tac tat tgc gct aaa gac    2705
Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp
                130                 135                 140

tat gaa ggt act ggt tat gct ttc gac ata tgg ggt caa ggt act atg    2753
Tyr Glu Gly Thr Gly Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
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gtc acc gtc tct agt gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg   2801
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        160                 165                 170

gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc   2849
Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
    175                 180                 185

ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca   2897
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
190                 195                 200                 205

ggc gcc ctg acc agc ggc gtc cac acc ttc ccg gct gtc cta cag tct   2945
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                210                 215                 220

agc gga ctc tac tcc ctc agc agc gta gtg acc gtg ccc tct tct agc   2993
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            225                 230                 235

ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac   3041
Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
        240                 245                 250

acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gcg gcc gct cat   3089
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Ala Ala Ala His
    255                 260                 265

cac cac cat cat cac tct gct gaa caa aaa ctc atc tca gaa gag gat   3137
His His His His His Ser Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp
270                 275                 280                 285

ctg aat ggt gcc gca gat atc aac gat gat cgt atg gct ggc gcc gct   3185
Leu Asn Gly Ala Ala Asp Ile Asn Asp Asp Arg Met Ala Gly Ala Ala
                290                 295                 300

gaa act gtt gaa agt tgt tta gca aaa ccc cat aca gaa aat tca ttt   3233
Glu Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe
            305                 310                 315

act aac gtc tgg aaa gac gac aaa act tta gat cgt tac gct aac tat   3281
Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr
        320                 325                 330

gag ggt tgt ctg tgg aat gct aca ggc gtt gta gtt tgt act ggt gac   3329
Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys Thr Gly Asp
    335                 340                 345

gaa act cag tgt tac ggt aca tgg gtt cct att ggg ctt gct atc cct   3377
Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro
350                 355                 360                 365

gaa aat gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggt   3425
Glu Asn Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
                370                 375                 380
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Ser Glu Gly Gly Gly Thr
            385

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aataataggt tccgaaatag gcaggggggca ttaactgttt atacgggcac tgttactcaa 3653

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ggttctgagg gtggcggctc tgagggaggc ggttccggtg gtggctctgg t tcc ggt  3950
                                                        Ser Gly

gat ttt gat tat gaa aag atg gca aac gct aat aag ggg gct atg acc   3998
Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr
390                 395                 400                 405

gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt   4046
Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu
                410                 415                 420

gat tct gtc gct act gat tac ggt gct gct atc gat ggt ttc att ggt   4094
Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly
            425                 430                 435

gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt gat ttt gct   4142
Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala
        440                 445                 450

ggc tct aat tcc caa atg gct caa gtc ggt gac ggt gat aat tca cct   4190
Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro
    455                 460                 465

tta atg aat aat ttc cgt caa tat tta cct tcc ctc cct caa tcg gtt   4238
Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val
470                 475                 480                 485

gaa tgt cgc cct ttt gtc ttt agc gct ggt aaa cca tat gaa ttt tct   4286
Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser
                490                 495                 500

att gat tgt gac aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt   4334
Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu
            505                 510                 515

tta tat gtt gcc acc ttt atg tat gta ttt tct acg ttt gct aac ata   4382
Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile
        520                 525                 530

ctg cgt aat aag gag tct taatc atg cca gtt ctt ttg ggt att ccg tta 4432
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Leu Arg Asn Lys Glu Ser        Met Pro Val Leu Leu Gly Ile Pro Leu
    535                        540                 545

tta ttg cgt ttc ctc ggt ttccttctgg taactttgtt cggctatctg          4480
Leu Leu Arg Phe Leu Gly
    550

cttacttttc ttaaaaaggg cttcggtaag atagctattg ctatttcatt gtttcttgct 4540

cttattattg ggcttaactc aattcttgtg ggttatctct ctgatattag cgctcaatta 4600

ccctctgact ttgttcaggg tgttcagtta attctcccgt ctaatgcgct tccctgtttt 4660

tatgttattc tctctgtaaa ggctgctatt ttcatttttg acgttaaaca aaaaatcgtt 4720

tcttatttgg attgggataa ataat atg gct gtt tat ttt gta act ggc aaa   4772
                           Met Ala Val Tyr Phe Val Thr Gly Lys
                           555                 560

tta ggc tct gga aag acg ctc gtt agc gtt ggt aag att cag gat aaa   4820
Leu Gly Ser Gly Lys Thr Leu Val Ser Val Gly Lys Ile Gln Asp Lys
    565                 570                 575

att gta gct ggg tgc aaa ata gca act aat ctt gat tta agg ctt caa   4868
Ile Val Ala Gly Cys Lys Ile Ala Thr Asn Leu Asp Leu Arg Leu Gln
580                 585                 590                 595

aac ctc ccg caa gtc ggg agg ttc gct aaa acg cct cgc gtt ctt aga   4916
Asn Leu Pro Gln Val Gly Arg Phe Ala Lys Thr Pro Arg Val Leu Arg
                600                 605                 610

ata ccg gat aag cct tct ata tct gat ttg ctt gct att ggg cgc ggt   4964
Ile Pro Asp Lys Pro Ser Ile Ser Asp Leu Leu Ala Ile Gly Arg Gly
            615                 620                 625

aat gat tcc tac gat gaa aat aaa aac ggc ttg ctt gtt ctc gat gag   5012
Asn Asp Ser Tyr Asp Glu Asn Lys Asn Gly Leu Leu Val Leu Asp Glu
        630                 635                 640

tgc ggt act tgg ttt aat acc cgt tct tgg aat gat aag gaa aga cag   5060
Cys Gly Thr Trp Phe Asn Thr Arg Ser Trp Asn Asp Lys Glu Arg Gln
    645                 650                 655

ccg att att gat tgg ttt cta cat gct cgt aaa tta gga tgg gat att   5108
Pro Ile Ile Asp Trp Phe Leu His Ala Arg Lys Leu Gly Trp Asp Ile
660                 665                 670                 675

att ttt ctt gtt cag gac tta tct att gtt gat aaa cag gcg cgt tct   5156
Ile Phe Leu Val Gln Asp Leu Ser Ile Val Asp Lys Gln Ala Arg Ser
                680                 685                 690

gca tta gct gaa cat gtt gtt tat tgt cgt cgt ctg gac aga att act   5204
Ala Leu Ala Glu His Val Val Tyr Cys Arg Arg Leu Asp Arg Ile Thr
            695                 700                 705

tta cct ttt gtc ggt act tta tat tct ctt att act ggc tcg aaa atg   5252
Leu Pro Phe Val Gly Thr Leu Tyr Ser Leu Ile Thr Gly Ser Lys Met
        710                 715                 720
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cct ctg cct aaa tta cat gtt ggc gtt gtt aaa tat ggc gat tct caa   5300
Pro Leu Pro Lys Leu His Val Gly Val Val Lys Tyr Gly Asp Ser Gln
    725                 730                 735

tta agc cct act gtt gag cgt tgg ctt tat act ggt aag aat ttg tat   5348
Leu Ser Pro Thr Val Glu Arg Trp Leu Tyr Thr Gly Lys Asn Leu Tyr
740                 745                 750                 755

aac gca tat gat act aaa cag gct ttt tct agt aat tat gat tcc ggt   5396
Asn Ala Tyr Asp Thr Lys Gln Ala Phe Ser Ser Asn Tyr Asp Ser Gly
                760                 765                 770

gtt tat tct tat tta acg cct tat tta tca cac ggt cgg tat ttc aaa   5444
Val Tyr Ser Tyr Leu Thr Pro Tyr Leu Ser His Gly Arg Tyr Phe Lys
            775                 780                 785

cca tta aat tta ggt cag aag atg aaa tta act aaa ata tat ttg aaa   5492
Pro Leu Asn Leu Gly Gln Lys Met Lys Leu Thr Lys Ile Tyr Leu Lys
        790                 795                 800

aag ttt tct cgc gtt ctt tgt ctt gcg att gga ttt gca tca gca ttt   5540
Lys Phe Ser Arg Val Leu Cys Leu Ala Ile Gly Phe Ala Ser Ala Phe
    805                 810                 815

aca tat agt tat ata acc caa cct aag ccg gag gtt aaa aag gta gtc   5588
Thr Tyr Ser Tyr Ile Thr Gln Pro Lys Pro Glu Val Lys Lys Val Val
820                 825                 830                 835

tct cag acc tat gat ttt gat aaa ttc act att gac tct tct cag cgt   5636
Ser Gln Thr Tyr Asp Phe Asp Lys Phe Thr Ile Asp Ser Ser Gln Arg
                840                 845                 850

ctt aat cta agc tat cgc tat gtt ttc aag gat tct aag gga aaa tta   5684
Leu Asn Leu Ser Tyr Arg Tyr Val Phe Lys Asp Ser Lys Gly Lys Leu
            855                 860                 865

att aat agc gac gat tta cag aag caa ggt tat tca ctc aca tat att   5732
Ile Asn Ser Asp Asp Leu Gln Lys Gln Gly Tyr Ser Leu Thr Tyr Ile
        870                 875                 880

gat tta tgt act gtt tcc att aaa aaa ggt aat tca aat gaa att gtt   5780
Asp Leu Cys Thr Val Ser Ile Lys Lys Gly Asn Ser Asn Glu Ile Val
    885                 890                 895

aaa tgt aat taattttgtt ttcttgatgt ttgtttcatc atcttctttt           5829
Lys Cys Asn
900

gctcaggtaa ttgaaatgaa taattcgcct ctgcgcgatt ttgtaacttg gtattcaaag 5889

caatcaggcg aatccgttat tgtttctccc gatgtaaaag gtactgttac tgtatattca 5949

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tatattgatg aattgccatc atctgataat caggaatatg atgataattc cgctccttct 6129
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<210> 452
<211> 20
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: MALIA3 peptide sequence

<400> 452
Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
1 5 10 15

His Ser Ala Gln
20

<210> 453
<211> 367
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: MALIA3 protein sequence

<400> 453
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
20 25 30

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly
50 55 60

Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr
65 70 75 80

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Lys Asp Tyr Glu Gly Thr Gly Tyr Ala
115 120 125

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser
130 135 140

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
145 150 155 160

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro

```
                165                 170                 175

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
            180                 185                 190

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
        195                 200                 205

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
    210                 215                 220

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
225                 230                 235                 240

Glu Pro Lys Ser Cys Ala Ala Ala His His His His His His Ser Ala
                245                 250                 255

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala Asp Ile
            260                 265                 270

Asn Asp Asp Arg Met Ala Gly Ala Ala Glu Thr Val Glu Ser Cys Leu
        275                 280                 285

Ala Lys Pro His Thr Glu Asn Ser Phe Thr Asn Val Trp Lys Asp Asp
    290                 295                 300

Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala
305                 310                 315                 320

Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr
                325                 330                 335

Trp Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu Gly Gly Gly Ser
            340                 345                 350

Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Thr
        355                 360                 365


<210> 454
<211> 152
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: MALIA3 protein
      sequence

<400> 454
Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala
  1               5                  10                  15

Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly
             20                  25                  30

Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe
         35                  40                  45
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Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp
50 55 60

Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn
65 70 75 80

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
85 90 95

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu
100 105 110

Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala
115 120 125

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala
130 135 140

Asn Ile Leu Arg Asn Lys Glu Ser
145 150

<210> 455
<211> 15
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: MALIA3 peptide sequence

<400> 455
Met Pro Val Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly
1 5 10 15

<210> 456
<211> 348
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: MALIA3 protein sequence

<400> 456
Met Ala Val Tyr Phe Val Thr Gly Lys Leu Gly Ser Gly Lys Thr Leu
1 5 10 15

Val Ser Val Gly Lys Ile Gln Asp Lys Ile Val Ala Gly Cys Lys Ile
20 25 30

Ala Thr Asn Leu Asp Leu Arg Leu Gln Asn Leu Pro Gln Val Gly Arg
35 40 45

Phe Ala Lys Thr Pro Arg Val Leu Arg Ile Pro Asp Lys Pro Ser Ile
50 55 60

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Ser Asp Leu Leu Ala Ile Gly Arg Gly Asn Asp Ser Tyr Asp Glu Asn
 65                  70                  75                  80

Lys Asn Gly Leu Leu Val Leu Asp Glu Cys Gly Thr Trp Phe Asn Thr
                85                  90                  95

Arg Ser Trp Asn Asp Lys Glu Arg Gln Pro Ile Ile Asp Trp Phe Leu
            100                 105                 110

His Ala Arg Lys Leu Gly Trp Asp Ile Ile Phe Leu Val Gln Asp Leu
        115                 120                 125

Ser Ile Val Asp Lys Gln Ala Arg Ser Ala Leu Ala Glu His Val Val
    130                 135                 140

Tyr Cys Arg Arg Leu Asp Arg Ile Thr Leu Pro Phe Val Gly Thr Leu
145                 150                 155                 160

Tyr Ser Leu Ile Thr Gly Ser Lys Met Pro Leu Pro Lys Leu His Val
                165                 170                 175

Gly Val Val Lys Tyr Gly Asp Ser Gln Leu Ser Pro Thr Val Glu Arg
            180                 185                 190

Trp Leu Tyr Thr Gly Lys Asn Leu Tyr Asn Ala Tyr Asp Thr Lys Gln
        195                 200                 205

Ala Phe Ser Ser Asn Tyr Asp Ser Gly Val Tyr Ser Tyr Leu Thr Pro
    210                 215                 220

Tyr Leu Ser His Gly Arg Tyr Phe Lys Pro Leu Asn Leu Gly Gln Lys
225                 230                 235                 240

Met Lys Leu Thr Lys Ile Tyr Leu Lys Lys Phe Ser Arg Val Leu Cys
                245                 250                 255

Leu Ala Ile Gly Phe Ala Ser Ala Phe Thr Tyr Ser Tyr Ile Thr Gln
            260                 265                 270

Pro Lys Pro Glu Val Lys Lys Val Val Ser Gln Thr Tyr Asp Phe Asp
        275                 280                 285

Lys Phe Thr Ile Asp Ser Ser Gln Arg Leu Asn Leu Ser Tyr Arg Tyr
    290                 295                 300

Val Phe Lys Asp Ser Lys Gly Lys Leu Ile Asn Ser Asp Asp Leu Gln
305                 310                 315                 320

Lys Gln Gly Tyr Ser Leu Thr Tyr Ile Asp Leu Cys Thr Val Ser Ile
                325                 330                 335

Lys Lys Gly Asn Ser Asn Glu Ile Val Lys Cys Asn
            340                 345
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<210> 457
<211> 24
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 457
tggaagaggc acgttctttt cttt 24

<210> 458
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 458
cttttctttg ttgccgttgg ggtg 24

<210> 459
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 459
acactctccc ctgttgaagc tctt 24

<210> 460
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 460
accgcctcca ccgggcgcgc cttattaaca ctctcccctg ttgaagctct t 51

<210> 461
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 461
tgaacattct gtaggggcca ctg 23

<210> 462

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 462
agagcattct gcaggggcca ctg 23

<210> 463
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 463
accgcctcca ccgggcgcgc cttattatga acattctgta ggggccactg 50

<210> 464
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 464
accgcctcca ccgggcgcgc cttattaaga gcattctgca ggggccactg 50

<210> 465
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 465
cgactggagc acgaggacac tga 23

<210> 466
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 466
ggacactgac atggactgaa ggagta 26

<210> 467
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 467
gggaggatgg agactgggtc 20

<210> 468
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 468
gggaagatgg agactgggtc 20

<210> 469
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 469
gggagagtgg agactgagtc 20

<210> 470
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 470
gggtgcctgg agactgcgtc 20

<210> 471
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 471
gggtggctgg agactgcgtc 20

<210> 472
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 472
gggaggatgg agactgggtc atctggatgt cttgtgcact gtgacagagg 50

<210> 473
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 473
gggaagatgg agactgggtc atctggatgt cttgtgcact gtgacagagg 50

<210> 474
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 474
gggagagtgg agactgggtc atctggatgt cttgtgcact gtgacagagg 50

<210> 475
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 475
gggtgcctgg agactgggtc atctggatgt cttgtgcact gtgacagagg 50

<210> 476
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 476
gggtggctgg agactgggtc atctggatgt cttgtgcact gtgacagagg 50

<210> 477
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 477
gggagtctgg agactgggtc atctggatgt cttgtgcact gtgacagagg 50

<210> 478
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 478
cctctgtcac agtgcacaag acatccagat gacccagtct cc 42

<210> 479
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 479
cctctgtcac agtgcacaag ac 22

<210> 480
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 480
acactctccc ctgttgaagc tctt 24

<210> 481
<211> 668
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(668)

<400> 481
agt gca caa gac atc cag atg acc cag tct cca gcc acc ctg tct gtg 48
Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Val
1 5 10 15

tct cca ggg gaa agg gcc acc ctc tcc tgc agg gcc agt cag agt gtt 96
Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
20 25 30

agt aac aac tta gcc tgg tac cag cag aaa cct ggc cag gtt ccc agg 144
Ser Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Arg
35 40 45

ctc ctc atc tat ggt gca tcc acc agg gcc act gat atc cca gcc agg 192
Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Asp Ile Pro Ala Arg
50 55 60

ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga 240
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
65 70 75 80

ctg gag cct gaa gat ttt gca gtg tat tac tgt cag cgg tat ggt agc 288
Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Arg Tyr Gly Ser
85 90 95

tca ccg ggg tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga 336
Ser Pro Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag 384
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
115 120 125

ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat 432
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg 480
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc 528

```
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa   576
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190

cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg cct   624
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205

gtc aca aag agc ttc aac aaa gga gag tgt aag ggc gaa ttc gc        668
Val Thr Lys Ser Phe Asn Lys Gly Glu Cys Lys Gly Glu Phe Ala
    210                 215                 220


<210> 482
<211> 223
<212> PRT
<213> Homo sapiens

<400> 482
Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Val
  1               5                  10                  15

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val
             20                  25                  30

Ser Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Arg
         35                  40                  45

Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Asp Ile Pro Ala Arg
     50                  55                  60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg
 65                  70                  75                  80

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Arg Tyr Gly Ser
                 85                  90                  95

Ser Pro Gly Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105                 110

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
        115                 120                 125

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
    130                 135                 140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145                 150                 155                 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
                165                 170                 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
            180                 185                 190
```

```
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
        195                 200                 205

Val Thr Lys Ser Phe Asn Lys Gly Glu Cys Lys Gly Glu Phe Ala
    210                 215                 220


<210> 483
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 483
agccaccctg tct                                                    13


<210> 484
<211> 700
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(699)

<400> 484
agt gca caa gac atc cag atg acc cag tct cct gcc acc ctg tct gtg   48
Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Val
  1               5                  10                  15

tct cca ggt gaa aga gcc acc ctc tcc tgc agg gcc agt cag gtg tct   96
Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Val Ser
             20                  25                  30

cca ggg gaa aga gcc acc ctc tcc tgc aat ctt ctc agc aac tta gcc   144
Pro Gly Glu Arg Ala Thr Leu Ser Cys Asn Leu Leu Ser Asn Leu Ala
         35                  40                  45

tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc atc tat ggt   192
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly
     50                  55                  60

gct tcc acc ggg gcc att ggt atc cca gcc agg ttc agt ggc agt ggg   240
Ala Ser Thr Gly Ala Ile Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
 65                  70                  75                  80

tct ggg aca gag ttc act ctc acc atc agc agc ctg cag tct gaa gat   288
Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp
                 85                  90                  95

ttt gca gtg tat ttc tgt cag cag tat ggt acc tca ccg ccc act ttc   336
Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Thr Ser Pro Pro Thr Phe
            100                 105                 110
```

```
ggc gga ggg acc aag gtg gag atc aaa cga act gtg gct gca cca tct   384
Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
        115                 120                 125

gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc   432
Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
    130                 135                 140

tct gtt gtg tgc ccg ctg aat aac ttc tat ccc aga gag gcc aaa gta   480
Ser Val Val Cys Pro Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
145                 150                 155                 160

cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt   528
Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
                165                 170                 175

gtc aca gag cag gac aac aag gac agc acc tac agc ctc agc agc acc   576
Val Thr Glu Gln Asp Asn Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
            180                 185                 190

ctg acg ctg agc aaa gta gac tac gag aaa cac gaa gtc tac gcc tgc   624
Leu Thr Leu Ser Lys Val Asp Tyr Glu Lys His Glu Val Tyr Ala Cys
        195                 200                 205

gaa gtc acc cat cag ggc ctt agc tcg ccc gtc acg aag agc ttc aac   672
Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
    210                 215                 220

agg gga gag tgt aag aaa gaa ttc gtt t                            700
Arg Gly Glu Cys Lys Lys Glu Phe Val
225                 230
```

<210> 485
<211> 233
<212> PRT
<213> Homo sapiens

<400> 485

```
Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Val
  1               5                  10                  15

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Val Ser
            20                  25                  30

Pro Gly Glu Arg Ala Thr Leu Ser Cys Asn Leu Leu Ser Asn Leu Ala
        35                  40                  45

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly
    50                  55                  60

Ala Ser Thr Gly Ala Ile Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly
65                  70                  75                  80

Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp
                85                  90                  95

Phe Ala Val Tyr Phe Cys Gln Gln Tyr Gly Thr Ser Pro Pro Thr Phe
```

```
            100                 105                 110

Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
        115                 120                 125

Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
    130                 135                 140

Ser Val Val Cys Pro Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val
145                 150                 155                 160

Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser
                165                 170                 175

Val Thr Glu Gln Asp Asn Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr
            180                 185                 190

Leu Thr Leu Ser Lys Val Asp Tyr Glu Lys His Glu Val Tyr Ala Cys
        195                 200                 205

Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
    210                 215                 220

Arg Gly Glu Cys Lys Lys Glu Phe Val
225                 230
```

<210> 486
<211> 419
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 3-23
VH nucleotide sequence

<220>
<221> CDS
<222> (12)..(419)

<400> 486

```
ctgtctgaac g gcc cag ccg gcc atg gcc gaa gtt caa ttg tta gag tct  50
              Ala Gln Pro Ala Met Ala Glu Val Gln Leu Leu Glu Ser
                1               5                   10

ggt ggc ggt ctt gtt cag cct ggt ggt tct tta cgt ctt tct tgc gct   98
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
     15                  20                  25

gct tcc gga ttc act ttc tct tcg tac gct atg tct tgg gtt cgc caa   146
Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln
 30                  35                  40                  45

gct cct ggt aaa ggt ttg gag tgg gtt tct gct atc tct ggt tct ggt   194
Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly
                50                  55                  60
```

```
ggc agt act tac tat gct gac tcc gtt aaa ggt cgc ttc act atc tct   242
Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
            65                  70                  75

aga gac aac tct aag aat act ctc tac ttg cag atg aac agc tta agg   290
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
        80                  85                  90

gct gag gac act gca gtc tac tat tgc gct aaa gac tat gaa ggt act   338
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Tyr Glu Gly Thr
    95                  100                 105

ggt tat gct ttc gac ata tgg ggt caa ggt act atg gtc acc gtc tct   386
Gly Tyr Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
110                 115                 120                 125

agt gcc tcc acc aag ggc cca tcg gtc ttc ccc                       419
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
                130                 135
```

<210> 487
<211> 136
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic 3-23
VH protein sequence

<400> 487

```
Ala Gln Pro Ala Met Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
  1               5                  10                  15

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
            20                  25                  30

Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly
        35                  40                  45

Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr
    50                  55                  60

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
65                  70                  75                  80

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
                85                  90                  95

Thr Ala Val Tyr Tyr Cys Ala Lys Asp Tyr Glu Gly Thr Gly Tyr Ala
            100                 105                 110

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser
        115                 120                 125

Thr Lys Gly Pro Ser Val Phe Pro
    130                 135
```

<210> 488
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 488
ctgtctgaac ggcccagccg 20

<210> 489
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 489
ctgtctgaac ggcccagccg gccatggccg aagttcaatt gttagagtct ggtggcggtc 60
ttgttcagcc tggtggttct tta 83

<210> 490
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 490
gaaagtgaat ccggaagcag cgcaagaaag acgtaaagaa ccaccaggct gaac 54

<210> 491
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 491
agaaacccac tccaaacctt taccaggagc ttggcgaacc ca 42

<210> 492
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 492
agtgtcctca gcccttaagc tgttcatctg caagtagaga gtattcttag agttgtctct 60
agagatagtg aagcgacctt taacggagtc agca 94

<210> 493
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 493
gcttaagggc tgaggacact gcagtctact attgcgctaa agactatgaa ggtactggtt 60
atgctttcga catatggggt c 81

<210> 494
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 494
ggggaagacc gatgggccct tggtggaggc actagagacg gtgaccatag taccttgacc 60
tatgtcgaaa gc 72

<210> 495
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 495
ggggaagacc gatgggccct tgg 23

<210> 496
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (22)..(24)
<223> A, T, C, G, other or unknown

<220>
<221> modified_base
<222> (28)..(30)
<223> A, T, C, G, other or unknown

<220>
<221> modified_base
<222> (34)..(36)
<223> A, T, C, G, other or unknown

<220>
<223> nnn codes for any amino acid but Cys

<400> 496
gcttccggat tcactttctc tnnntacnnn atgnnntggg ttcgccaagc tcctgg 56

<210> 497
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (19)..(21)
<223> A, T, C or G

<220>
<221> modified_base
<222> (25)..(30)
<223> A, T, C or G

<220>
<221> modified_base
<222> (40)..(42)
<223> A, T, C or G

<220>
<221> modified_base
<222> (46)..(48)
<223> A, T, C or G

<400> 497
ggtttggagt gggtttctnn natcnnnnnn tctggtggcn nnactnnnta tgctgactcc 60
gttaaagg 68

<210> 498

<211> 912
<212> DNA
<213> Escherichia coli

<400> 498
tccggagctt cagatctgtt tgccttttg tggggtggtg cagatcgcgt tacggagatc 60
gaccgactgc ttgagcaaaa gccacgctta actgctgatc aggcatggga tgttattcgc 120
caaaccagtc gtcaggatct taacctgagg ctttttttac ctactctgca agcagcgaca 180
tctggtttga cacagagcga tccgcgtcgt cagttggtag aaacattaac acgttgggat 240
ggcatcaatt tgcttaatga tgatggtaaa acctggcagc agccaggctc tgccatcctg 300
aacgtttggc tgaccagtat gttgaagcgt accgtagtgg ctgccgtacc tatgccattt 360
gataagtggt acagcgccag tggctacgaa acaacccagg acggcccaac tggttcgctg 420
aatataagtg ttggagcaaa aattttgtat gaggcggtgc agggagacaa atcaccaatc 480
ccacaggcgg ttgatctgtt tgctgggaaa ccacagcagg aggttgtgtt ggctgcgctg 540
gaagatacct gggagactct ttccaaacgc tatggcaata atgtgagtaa ctggaaaaca 600
cctgcaatgg ccttaacgtt ccgggcaaat aatttctttg gtgtaccgca ggccgcagcg 660
gaagaaacgc gtcatcaggc ggagtatcaa aaccgtggaa cagaaaacga tatgattgtt 720
ttctcaccaa cgacaagcga tcgtcctgtg cttgcctggg atgtggtcgc acccggtcag 780
agtgggttta ttgctcccga tggaacagtt gataagcact atgaagatca gctgaaaatg 840
tacgaaaatt ttggccgtaa gtcgctctgg ttaacgaagc aggatgtgga ggcgcataag 900
gagtcgtcta ga 912

<210> 499
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (4)..(7)
<223> A, T, C, G, other or unknown

<400> 499
gatnnnnatc 10

<210> 500
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (1)..(15)
<223> A, T, C, G, other or unknown

<400> 500
nnnnnnnnnn nnnnngtccc 20

<210> 501
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(8)
<223> A, T, C, G, other or unknown

<400> 501
gcannnnntg c 11

<210> 502
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(7)
<223> A, T, C, G, other or unknown

<400> 502
gacnnnngtc 10

<210> 503
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (1)..(7)
<223> A, T, C, G, other or unknown

<400> 503
nnnnnnngcg gg 12

<210> 504
<211> 12
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(12)
<223> A, T, C, G, other or unknown

<400> 504
gtatccnnnn nn 12

<210> 505
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(9)
<223> A, T, C, G, other or unknown

<400> 505
gcannnnnnt cg 12

<210> 506
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(8)
<223> A, T, C, G, other or unknown

<400> 506
gccnnnnngg c 11

<210> 507
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<220>
<221> modified_base
<222> (7)..(11)
<223> A, T, C, G, other or unknown

<400> 507
ggtctcnnnn n 11

<210> 508
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(11)
<223> A, T, C, G, other or unknown

<400> 508
gacnnnnngt c 11

<210> 509
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(8)
<223> A, T, C, G, other or unknown

<400> 509
gacnnnnngt c 11

<210> 510
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base

<222> (4)..(9)
<223> A, T, C, G, other or unknown

<400> 510
gacnnnnnng tc 12

<210> 511
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(8)
<223> A, T, C, G, other or unknown

<400> 511
ccannnnntg g 11

<210> 512
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (1)..(9)
<223> A, T, C, G, other or unknown

<400> 512
nnnnnnnnng caggt 15

<210> 513
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(11)
<223> A, T, C, G, other or unknown

<400> 513

acctgcnnnn n 11

<210> 514
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (5)..(9)
<223> A, T, C, G, other or unknown

<400> 514
ggccnnnnng gcc 13

<210> 515
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(12)
<223> A, T, C, G, other or unknown

<400> 515
ccannnnnnn nntgg 15

<210> 516
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(11)
<223> A, T, C, G, other or unknown

<400> 516
cgtctcnnnn n 11

<210> 517

<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (1)..(6)
<223> A, T, C, G, other or unknown

<400> 517
nnnnnngaga cg 12

<210> 518
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (1)..(10)
<223> A, T, C, G, other or unknown

<400> 518
nnnnnnnnnn ctcctc 16

<210> 519
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(16)
<223> A, T, C, G, other or unknown

<400> 519
gaggagnnnn nnnnnn 16

<210> 520
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(8)
<223> A, T, C, G, other or unknown

<400> 520
cctnnnnnag g 11

<210> 521
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (4)..(9)
<223> A, T, C, G, other or unknown

<400> 521
ccannnnnnt gg 12

<210> 522
<211> 6680
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vector pCES5 nucleotide sequence

<220>
<221> CDS
<222> (201)..(1058)

<220>
<221> CDS
<222> (2269)..(2682)

<220>
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<222> (4198)..(5799)

<400> 522

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gacgaaaggg cctcgtgata cgcctatttt tataggttaa tgtcatgata ataatggttt 60

cttagacgtc aggtggcact tttcggggaa atgtgcgcgg aacccctatt tgtttatttt 120

tctaaataca ttcaaatatg tatccgctca tgagacaata accctgataa atgcttcaat 180

aatattgaaa aaggaagagt atg agt att caa cat ttc cgt gtc gcc ctt att 233
                       Met Ser Ile Gln His Phe Arg Val Ala Leu Ile
                         1               5                  10

ccc ttt ttt gcg gca ttt tgc ctt cct gtt ttt gct cac cca gaa acg   281
Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr
            15                  20                  25

ctg gtg aaa gta aaa gat gct gaa gat cag ttg ggt gcc cga gtg ggt   329
Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly
        30                  35                  40

tac atc gaa ctg gat ctc aac agc ggt aag atc ctt gag agt ttt cgc   377
Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg
    45                  50                  55

ccc gaa gaa cgt ttt cca atg atg agc act ttt aaa gtt ctg cta tgt   425
Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys
60                  65                  70                  75

ggc gcg gta tta tcc cgt att gac gcc ggg caa gag caa ctc ggt cgc   473
Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg
                80                  85                  90

cgc ata cac tat tct cag aat gac ttg gtt gag tac tca cca gtc aca   521
Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr
            95                  100                 105

gaa aag cat ctt acg gat ggc atg aca gta aga gaa tta tgc agt gct   569
Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala
        110                 115                 120

gcc ata acc atg agt gat aac act gcg gcc aac tta ctt ctg aca acg   617
Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr
    125                 130                 135

atc gga gga ccg aag gag cta acc gct ttt ttg cac aac atg ggg gat   665
Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp
140                 145                 150                 155

cat gta act cgc ctt gat cgt tgg gaa ccg gag ctg aat gaa gcc ata   713
His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile
                160                 165                 170

cca aac gac gag cgt gac acc acg atg cct gta gca atg gca aca acg   761
Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr
            175                 180                 185

ttg cgc aaa cta tta act ggc gaa cta ctt act cta gct tcc cgg caa   809
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Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln
        190                 195                 200

caa tta ata gac tgg atg gag gcg gat aaa gtt gca gga cca ctt ctg   857
Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu
    205                 210                 215

cgc tcg gcc ctt ccg gct ggc tgg ttt att gct gat aaa tct gga gcc   905
Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala
220                 225                 230                 235

ggt gag cgt ggg tct cgc ggt atc att gca gca ctg ggg cca gat ggt   953
Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly
                240                 245                 250

aag ccc tcc cgt atc gta gtt atc tac acg acg ggg agt cag gca act   1001
Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr
            255                 260                 265

atg gat gaa cga aat aga cag atc gct gag ata ggt gcc tca ctg att   1049
Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile
        270                 275                 280

aag cat tgg taactgtcag accaagttta ctcatatata ctttagattg           1098
Lys His Trp
    285

atttaaaact tcatttttaa tttaaaagga tctaggtgaa gatccttttt gataatctca 1158

tgaccaaaat cccttaacgt gagttttcgt tccactgagc gtcagacccc gtagaaaaga 1218

tcaaaggatc ttcttgagat cctttttttc tgcgcgtaat ctgctgcttg caaacaaaaa 1278

aaccaccgct accagcggtg gtttgtttgc cggatcaaga gctaccaact ctttttccga 1338

aggtaactgg cttcagcaga gcgcagatac caaatactgt ccttctagtg tagccgtagt 1398

taggccacca cttcaagaac tctgtagcac cgcctacata cctcgctctg ctaatcctgt 1458

taccagtggc tgctgccagt ggcgataagt cgtgtcttac cgggttggac tcaagacgat 1518

agttaccgga taaggcgcag cggtcgggct gaacgggggg ttcgtgcata cagcccagct 1578

tggagcgaac gacctacacc gaactgagat acctacagcg tgagcattga gaaagcgcca 1638

cgcttcccga agggagaaag gcggacaggt atccggtaag cggcagggtc ggaacaggag 1698

agcgcacgag ggagcttcca gggggaaacg cctggtatct ttatagtcct gtcgggtttc 1758

gccacctctg acttgagcgt cgatttttgt gatgctcgtc agggggggcgg agcctatgga 1818

aaaacgccag caacgcggcc tttttacggt tcctggcctt ttgctggcct tttgctcaca 1878

tgttctttcc tgcgttatcc cctgattctg tggataaccg tattaccgcc tttgagtgag 1938

ctgataccgc tcgccgcagc cgaacgaccg agcgcagcga gtcagtgagc gaggaagcgg 1998

aagagcgccc aatacgcaaa ccgcctctcc ccgcgcgttg gccgattcat taatgcagct 2058
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ggcacgacag gtttcccgac tggaaagcgg gcagtgagcg caacgcaatt aatgtgagtt 2118

agctcactca ttaggcaccc caggctttac actttatgct tccggctcgt atgttgtgtg 2178

gaattgtgag cggataacaa tttcacacag gaaacagcta tgaccatgat tacgccaagc 2238

tttggagcct tttttttgga gattttcaac gtg aaa aaa tta tta ttc gca att  2292
                               Met Lys Lys Leu Leu Phe Ala Ile
                                               290

cct tta gtt gtt cct ttc tat tct cac agt gca cag gtc caa ctg cag   2340
Pro Leu Val Val Pro Phe Tyr Ser His Ser Ala Gln Val Gln Leu Gln
295                 300                 305                 310

gtc gac ctc gag atc aaa cgt gga act gtg gct gca cca tct gtc ttc   2388
Val Asp Leu Glu Ile Lys Arg Gly Thr Val Ala Ala Pro Ser Val Phe
                315                 320                 325

atc ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt   2436
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
            330                 335                 340

gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg   2484
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
        345                 350                 355

aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca   2532
Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
    360                 365                 370

gag cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg   2580
Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
375                 380                 385                 390

ctg agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc   2628
Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
                395                 400                 405

acc cat cag ggc ctg agt tca ccg gtg aca aag agc ttc aac agg gga   2676
Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
            410                 415                 420

gag tgt taataaggcg cgccaattct atttcaagga gacagtcata atg aaa tac   2731
Glu Cys                                             Met Lys Tyr
                                                    425

cta ttg cct acg gca gcc gct gga ttg tta tta ctc gcg gcc cag ccg   2779
Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro
        430                 435                 440

gcc atg gcc gaa gtt caa ttg tta gag tct ggt ggc ggt ctt gtt cag   2827
Ala Met Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
    445                 450                 455

cct ggt ggt tct tta cgt ctt tct tgc gct gct tcc gga gcttcagatc    2876
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala S r Gly
460                 465                 470
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tgtttgcctt tttgtggggt ggtgcagatc gcgttacgga gatcgaccga ctgcttgagc 2936

aaaagccacg cttaactgct gatcaggcat gggatgttat tcgccaaacc agtcgtcagg 2996

atcttaacct gaggcttttt ttacctactc tgcaagcagc gacatctggt ttgacacaga 3056

gcgatccgcg tcgtcagttg gtagaaacat taacacgttg ggatggcatc aatttgctta 3116

atgatgatgg taaaacctgg cagcagccag gctctgccat cctgaacgtt tggctgacca 3176

gtatgttgaa gcgtaccgta gtggctgccg tacctatgcc atttgataag tggtacagcg 3236

ccagtggcta cgaaacaacc caggacggcc caactggttc gctgaatata agtgttggag 3296

caaaaatttt gtatgaggcg gtgcagggag acaaatcacc aatcccacag gcggttgatc 3356

tgtttgctgg gaaaccacag caggaggttg tgttggctgc gctggaagat acctgggaga 3416

ctctttccaa acgctatggc aataatgtga gtaactggaa aacacctgca atggccttaa 3476

cgttccgggc aaataatttc tttggtgtac cgcaggccgc agcggaagaa acgcgtcatc 3536

aggcggagta tcaaaaccgt ggaacagaaa acgatatgat tgttttctca ccaacgacaa 3596

gcgatcgtcc tgtgcttgcc tgggatgtgg tcgcacccgg tcagagtggg tttattgctc 3656

ccgatggaac agttgataag cactatgaag atcagctgaa aatgtacgaa aattttggcc 3716

gtaagtcgct ctggttaacg aagcaggatg tggaggcgca taaggagtcg tct aga     3772
                                                        Ser Arg

gac aac tct aag aat act ctc tac ttg cag atg aac agc tta agt ctg    3820
Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Ser Leu
475                 480                 485                 490

agc att cgg tcc ggg caa cat tct cca aac tgaccagacg acacaaacgg      3870
Ser Ile Arg Ser Gly Gln His Ser Pro Asn
                495                 500

cttacgctaa atcccgcgca tgggatggta aagaggtggc gtctttgctg gcctggactc 3930

atcagatgaa ggccaaaaat tggcaggagt ggacacagca ggcagcgaaa caagcactga 3990

ccatcaactg gtactatgct gatgtaaacg gcaatattgg ttatgttcat actggtgctt 4050

atccagatcg tcaatcaggc catgatccgc gattacccgt tcctggtacg ggaaaatggg 4110

actggaaagg gctattgcct tttgaaatga accctaaggt gtataacccc cagaagctag 4170

cctgcggctt cggtcaccgt ctcaagc gcc tcc acc aag ggc cca tcg gtc ttc 4224
                              Ala Ser Thr Lys Gly Pro Ser Val Phe
                                                  505

ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg    4272
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
510                 515                 520                 525
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ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg   4320
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
                530                 535                 540

aac tca ggc gcc ctg acc agc ggc gtc cac acc ttc ccg gct gtc cta   4368
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
            545                 550                 555

cag tcc tca gga ctc tac tcc ctc agc agc gta gtg acc gtg ccc tcc   4416
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
        560                 565                 570

agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc   4464
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
    575                 580                 585

agc aac acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gcg gcc   4512
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Ala Ala
590                 595                 600                 605

gca cat cat cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca   4560
Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
                610                 615                 620

gaa gag gat ctg aat ggg gcc gca tag act gtt gaa agt tgt tta gca   4608
Glu Glu Asp Leu Asn Gly Ala Ala     Thr Val Glu Ser Cys Leu Ala
            625                 630                 635

aaa cct cat aca gaa aat tca ttt act aac gtc tgg aaa gac gac aaa   4656
Lys Pro His Thr Glu Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys
            640                 645                 650

act tta gat cgt tac gct aac tat gag ggc tgt ctg tgg aat gct aca   4704
Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr
        655                 660                 665

ggc gtt gtg gtt tgt act ggt gac gaa act cag tgt tac ggt aca tgg   4752
Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp
    670                 675                 680

gtt cct att ggg ctt gct atc cct gaa aat gag ggt ggt ggc tct gag   4800
Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu Gly Gly Gly Ser Glu
685                 690                 695                 700

ggt ggc ggt tct gag ggt ggc ggt tct gag ggt ggc ggt act aaa cct   4848
Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Thr Lys Pro
                705                 710                 715

cct gag tac ggt gat aca cct att ccg ggc tat act tat atc aac cct   4896
Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro
            720                 725                 730

ctc gac ggc act tat ccg cct ggt act gag caa aac ccc gct aat cct   4944
Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro
        735                 740                 745

aat cct tct ctt gag gag tct cag cct ctt aat act ttc atg ttt cag   4992
Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln
```

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    750                 755                 760

aat aat agg ttc cga aat agg cag ggt gca tta act gtt tat acg ggc   5040
Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly
765                 770                 775                 780

act gtt act caa ggc act gac ccc gtt aaa act tat tac cag tac act   5088
Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr
                785                 790                 795

cct gta tca tca aaa gcc atg tat gac gct tac tgg aac ggt aaa ttc   5136
Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe
            800                 805                 810

aga gac tgc gct ttc cat tct ggc ttt aat gag gat cca ttc gtt tgt   5184
Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys
        815                 820                 825

gaa tat caa ggc caa tcg tct gac ctg cct caa cct cct gtc aat gct   5232
Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala
    830                 835                 840

ggc ggc ggc tct ggt ggt ggt tct ggt ggc ggc tct gag ggt ggc ggc   5280
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly
845                 850                 855                 860

tct gag ggt ggc ggt tct gag ggt ggc ggc tct gag ggt ggc ggt tcc   5328
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
                865                 870                 875

ggt ggc ggc tcc ggt tcc ggt gat ttt gat tat gaa aaa atg gca aac   5376
Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn
            880                 885                 890

gct aat aag ggg gct atg acc gaa aat gcc gat gaa aac gcg cta cag   5424
Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln
        895                 900                 905

tct gac gct aaa ggc aaa ctt gat tct gtc gct act gat tac ggt gct   5472
Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala
    910                 915                 920

gct atc gat ggt ttc att ggt gac gtt tcc ggc ctt gct aat ggt aat   5520
Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn
925                 930                 935                 940

ggt gct act ggt gat ttt gct ggc tct aat tcc caa atg gct caa gtc   5568
Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val
                945                 950                 955

ggt gac ggt gat aat tca cct tta atg aat aat ttc cgt caa tat tta   5616
Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu
            960                 965                 970

cct tct ttg cct cag tcg gtt gaa tgt cgc cct tat gtc ttt ggc gct   5664
Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Tyr Val Phe Gly Ala
        975                 980                 985
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ggt aaa cca tat gaa ttt tct att gat tgt gac aaa ata aac tta ttc   5712
Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe
    990                 995                1000

cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc acc ttt atg tat gta   5760
Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val
1005               1010                1015                1020

ttt tcg acg ttt gct aac ata ctg cgt aat aag gag tct taataagaat    5809
Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
               1025                1030

tcactggccg tcgttttaca acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat 5869

cgccttgcag cacatccccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat 5929

cgcccttccc aacagttgcg cagcctgaat ggcgaatggc gcctgatgcg gtattttctc 5989

cttacgcatc tgtgcggtat ttcacaccgc atataaattg taaacgttaa tattttgtta 6049

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aaaatccctt ataaatcaaa agaatagccc gagatagggt tgagtgttgt tccagtttgg 6169

aacaagagtc cactattaaa gaacgtggac tccaacgtca aagggcgaaa aaccgtctat 6229

cagggcgatg gcccactacg tgaaccatca cccaaatcaa gttttttggg gtcgaggtgc 6289

cgtaaagcac taaatcggaa ccctaaaggg agcccccgat ttagagcttg acggggaaag 6349

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cagggcgcgt actatggttg ctttgacggg tgcagtctca gtacaatctg ctctgatgcc 6529

gcatagttaa gccagccccg acacccgcca acacccgctg acgcgccctg acgggcttgt 6589

ctgctcccgg catccgctta cagacaagct gtgaccgtct ccgggagctg catgtgtcag 6649

aggttttcac cgtcatcacc gaaacgcgcg a                                  6680
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<210> 523
<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vector pCES5
protein sequence

<400> 523

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Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
  1               5                  10                  15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
            20                  25                  30
```

```
Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
         35                  40                  45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
     50                  55                  60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65                  70                  75                  80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
                 85                  90                  95

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
            100                 105                 110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
        115                 120                 125

Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
    130                 135                 140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
145                 150                 155                 160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
                165                 170                 175

Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
            180                 185                 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
        195                 200                 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
    210                 215                 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
225                 230                 235                 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
                245                 250                 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
            260                 265                 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
        275                 280                 285


<210> 524
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vector pCES5
      protein sequence
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<400> 524
Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
1 5 10 15

His Ser Ala Gln Val Gln Leu Gln Val Asp Leu Glu Ile Lys Arg Gly
20 25 30

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
35 40 45

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
50 55 60

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
65 70 75 80

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
85 90 95

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
100 105 110

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
115 120 125

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
130 135

<210> 525
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vector pCES5 protein sequence

<400> 525
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
20 25 30

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

<210> 526
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vector pCES5

protein sequence

<400> 526
Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
1 5 10 15

Ser Leu Ser Ile Arg Ser Gly Gln His Ser Pro Asn
20 25

<210> 527
<211> 533
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vector pCES5 protein sequence

<400> 527
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Ala Ala Ala His His His His His His
100 105 110

Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
115 120 125

Ala Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe
130 135 140

Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr
145 150 155 160

Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys Thr Gly Asp
165 170 175

Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro
180 185 190

Glu Asn Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
195 200 205

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Ser Glu Gly Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile
    210                 215                 220

Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly
225                 230                 235                 240

Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln
                245                 250                 255

Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln
            260                 265                 270

Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro
        275                 280                 285

Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr
    290                 295                 300

Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly
305                 310                 315                 320

Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp
                325                 330                 335

Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly Gly Gly Ser
            340                 345                 350

Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
        355                 360                 365

Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp
    370                 375                 380

Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu
385                 390                 395                 400

Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp
                405                 410                 415

Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp
            420                 425                 430

Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly
        435                 440                 445

Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu
    450                 455                 460

Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu
465                 470                 475                 480

Cys Arg Pro Tyr Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile
                485                 490                 495

Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu
            500                 505                 510
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Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu
515 520 525

Arg Asn Lys Glu Ser
530

<210> 528
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 528
acctcactgg cttccggatt cactttctct 30

<210> 529
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 529
agaaacccac tccaaacctt taccaggagc ttggcgaacc ca 42

<210> 530
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 530
ggaaggcagt gatctagaga tagtgaagcg acctttaacg gagtcagcat a 51

<210> 531
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 531
ggaaggcagt gatctagaga tag 23

<210> 532
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 532
gtgctgactc agccaccctc 20

<210> 533
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 533
gccctgactc agcctgcctc 20

<210> 534
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 534
gagctgactc aggaccctgc 20

<210> 535
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 535
gagctgactc agccaccctc 20

<210> 536
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 536
cctcgacagc gaagtgcaca gagcgtcttg actcagcc 38

<210> 537
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 537
cctcgacagc gaagtgcaca gagcgtcttg 30

<210> 538
<211> 38
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 538
cctcgacagc gaagtgcaca gagcgctttg actcagcc 38

<210> 539
<211> 30
<212> DNA
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<220>
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<400> 539
cctcgacagc gaagtgcaca gagcgctttg 30

<210> 540
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 540
cctcgacagc taagtgcaca gagcgctttg actcagcc 38

<210> 541
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 541
cctcgacagc gaagtgcaca gagcgctttg 30

<210> 542
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 542
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<210> 543
<211> 30
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 543
cctcgacagc gaagtgcaca gagcgaattg 30

<210> 544
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 544
cctcgacagc gaagtgcaca gtacgaattg actcagcc 38

<210> 545
<211> 30
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 545
cctcgacagc gaagtgcaca gtacgaattg 30

<210> 546
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 546
cctcgacagc gaagtgcaca g 21

<210> 547
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 547
ccgtgtatta ctgtgcgaga g 21

<210> 548
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 548
ctgtgtatta ctgtgcgaga g 21

<210> 549
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 549

ccgtatatta ctgtgcgaaa g 21

<210> 550
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 550
ctgtgtatta ctgtgcgaaa g 21

<210> 551
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 551
ctgtgtatta ctgtgcgaga c 21

<210> 552
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 552
ccatgtatta ctgtgcgaga c 21

<210> 553
<211> 94
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 553
ggtgtagtga tctagtgaca actctaagaa tactctctac ttgcagatga acagctttag 60
ggctgaggac actgcagtct actattgtgc gaga 94

<210> 554
<211> 94

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 554
ggtgtagtga tctagtgaca actctaagaa tactctctac ttgcagatga acagctttag 60
ggctgaggac actgcagtct actattgtgc gaaa 94

<210> 555
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 555
atagtagact gcagtgtcct cagcccttaa gctgttcatc tgcaagtaga gagtattctt 60
agagttgtct ctagatcact acacc 85

<210> 556
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 556
gactgggtgt agtgatctag 20

<210> 557
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 557
cttttctttg ttgccgttgg ggtg 24

<210> 558
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
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<222> (1)..(9)
<223> A, T, C, G, other or unknown

<400> 558
nnnnnnnnng caggt 15

<210> 559
<211> 11
<212> DNA
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<220>
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<223> A, T, C, G, other or unknown

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acctgcnnnn n 11

<210> 560
<211> 10
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<221> modified_base
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<223> A, T, C, G, other or unknown

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gatnnnnatc 10

<210> 561
<211> 16
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<223> A, T, C, G, other or unknown

<400> 561
gaggagnnnn nnnnnn 16

<210> 562
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (1)..(10)
<223> A, T, C, G, other or unknown

<400> 562
nnnnnnnnnn ctcctc 16

<210> 563
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<223> A, T, C, G, other or unknown

<400> 563
ctcttcnnnn 10

<210> 564
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (1)..(5)
<223> A, T, C, G, other or unknown

<400> 564
nnnnngaaga g 11

<210> 565
<211> 20
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
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<223> A, T, C, G, other or unknown

<400> 565
nnnnnnnnnn nnnnngtccc 20

<210> 566
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<222> (4)..(9)
<223> A, T, C, G, other or unknown

<400> 566
gacnnnnnng tc 12

<210> 567
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<221> modified_base
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<223> A, T, C, G, other or unknown

<400> 567
cgtctcnnnn n 11

<210> 568
<211> 12

<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<223> A, T, C, G, other or unknown

<400> 568
gtatccnnnn nn 12

<210> 569
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<223> A, T, C, G, other or unknown

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<210> 570
<211> 11
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<222> (4)..(8)
<223> A, T, C, G, other or unknown

<400> 570
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<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
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<223> A, T, C, G, other or unknown

<400> 571
ggtctcnnnn n 11

<210> 572
<211> 11
<212> DNA
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<223> A, T, C, G, other or unknown

<400> 572
gacnnnnngt c 11

<210> 573
<211> 11
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<222> (4)..(8)
<223> A, T, C, G, other or unknown

<400> 573
gacnnnnngt c 11

<210> 574
<211> 11
<212> DNA
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<221> modified_base
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<223> A, T, C, G, other or unknown

<400> 574
ccannnnntg g 11

<210> 575
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<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<223> A, T, C, G, other or unknown

<400> 575
ccannnnnnn nntgg 15

<210> 576
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<222> (5)..(9)
<223> A, T, C, G, other or unknown

<400> 576
ggccnnnnng gcc 13

<210> 577
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<222> (4)..(9)
<223> A, T, C, G, other or unknown

<400> 577
ccannnnnnt gg 12

<210> 578
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<223> A, T, C, G, other or unknown

<400> 578
cctnnnnnag g 11

<210> 579
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<220>
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<220>
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<223> A, T, C, G, other or unknown

<400> 579
gacnnnngtc 10

<210> 580
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<220>
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<220>
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<223> A, T, C, G, other or unknown

<400> 580
ccannnnnnn nntgg 15

<210> 581
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<220>
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<220>
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<222> (4)..(8)
<223> A, T, C, G, other or unknown

<400> 581
gcannnnntg c 11

<210> 582
<211> 10251
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<220>
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<222> (8160)..(9452)

<400> 582
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atagctaaac aggttattga ccatttgcga aatgtatcta atggtcaaac taaatctact 120

cgttcgcaga attgggaatc aactgttata tggaatgaaa cttccagaca ccgtacttta 180

gttgcatatt taaaacatgt tgagctacag cattatattc agcaattaag ctctaagcca 240

tccgcaaaaa tgacctctta tcaaaaggag caattaaagg tactctctaa tcctgacctg 300

ttggagtttg cttccggtct ggttcgcttt gaagctcgaa ttaaaacgcg atatttgaag 360

tctttcgggc ttcctcttaa tctttttgat gcaatccgct ttgcttctga ctataatagt 420

cagggtaaag acctgatttt tgatttatgg tcattctcgt tttctgaact gtttaaagca 480

tttgaggggg attcaatgaa tatttatgac gattccgcag tattggacgc tatccagtct 540

aaacatttta ctattacccc ctctggcaaa acttcttttg caaaagcctc tcgctatttt 600

ggtttttatc gtcgtctggt aaacgagggt tatgatagtg ttgctcttac tatgcctcgt 660

aattcctttt ggcgttatgt atctgcatta gttgaatgtg gtattcctaa atctcaactg 720

atgaatcttt ctacctgtaa taatgttgtt ccgttagttc gttttattaa cgtagatttt 780

tcttcccaac gtcctgactg gtataatgag ccagttctta aaatcgcata aggtaattca 840

caatgattaa agttgaaatt aaaccatctc aagcccaatt tactactcgt tctggtgttt 900

ctcgtcaggg caagccttat tcactgaatg agcagctttg ttacgttgat ttgggtaatg 960

aatatccggt tcttgtcaag attactcttg atgaaggtca gccagcctat gcgcctggtc 1020

tgtacaccgt tcatctgtcc tctttcaaag ttggtcagtt cggttccctt atgattgacc 1080

gtctgcgcct cgttccggct aagtaacatg gagcaggtcg cggatttcga cacaatttat 1140

caggcgatga tacaaatctc cgttgtactt tgtttcgcgc ttggtataat cgctgggggt 1200

caaagatgag tgttttagtg tattcttttg cctctttcgt tttaggttgg tgccttcgta 1260

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caaagcctct gtagccgttg ctaccctcgt tccgatgctg tctttcgctg ctgagggtga 1380

cgatcccgca aaagcggcct ttaactccct gcaagcctca gcgaccgaat atatcggtta 1440

tgcgtgggcg atggttgttg tcattgtcgg cgcaactatc ggtatcaagc tgtttaagaa 1500

attcacctcg aaagcaagct gataaaccga tacaattaaa ggctcctttt ggagcctttt 1560

ttttggagat tttcaac gtg aaa aaa tta tta ttc gca att cct tta gtt 1610
Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val
1 5 10

gtt cct ttc tat tct ggc gcg gcc gaa tca cat cta gac ggc gcc gct 1658
Val Pro Phe Tyr Ser Gly Ala Ala Glu Ser His Leu Asp Gly Ala Ala
15 20 25

gaa act gtt gaa agt tgt tta gca aaa tcc cat aca gaa aat tca ttt 1706
Glu Thr Val Glu Ser Cys Leu Ala Lys Ser His Thr Glu Asn Ser Phe
30 35 40

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act aac gtc tgg aaa gac gac aaa act tta gat cgt tac gct aac tat   1754
Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr
     45                  50                  55

gag ggc tgt ctg tgg aat gct aca ggc gtt gta gtt tgt act ggt gac   1802
Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys Thr Gly Asp
 60                  65                  70                  75

gaa act cag tgt tac ggt aca tgg gtt cct att ggg ctt gct atc cct   1850
Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro
                 80                  85                  90

gaa aat gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggt   1898
Glu Asn Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
             95                  100                 105

tct gag ggt ggc ggt act aaacctcctg agtacggtga tacacctatt          1946
Ser Glu Gly Gly Gly Thr
        110

ccgggctata cttatatcaa ccctctcgac ggcacttatc cgcctggtac tgagcaaaac 2006

cccgctaatc ctaatccttc tcttgaggag tctcagcctc ttaatacttt catgtttcag 2066

aataataggt tccgaaatag gcaggggggca ttaactgttt atacgggcac tgttactcaa 2126

ggcactgacc ccgttaaaac ttattaccag tacactcctg tatcatcaaa agccatgtat 2186

gacgcttact ggaacggtaa attcagagac tgcgctttcc attctggctt taatgaggat 2246

ttatttgttt gtgaatatca aggccaatcg tctgacctgc ctcaacctcc tgtcaatgct 2306

ggcggcggct ctggtggtgg ttctggtggc ggctctgagg gtggtggctc tgagggaggc 2366

ggttccggtg gtggctctgg t tcc ggt gat ttt gat tat gaa aag atg gca   2417
                        Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala
                            115                 120

aac gct aat aag ggg gct atg acc gaa aat gcc gat gaa aac gcg cta   2465
Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu
    125                 130                 135

cag tct gac gct aaa ggc aaa ctt gat tct gtc gct act gat tac ggt   2513
Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly
140                 145                 150                 155

gct gct atc gat ggt ttc att ggt gac gtt tcc ggc ctt gct aat ggt   2561
Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly
                160                 165                 170

aat ggt gct act ggt gat ttt gct ggc tct aat tcc caa atg gct caa   2609
Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln
            175                 180                 185

gtc ggt gac ggt gat aat tca cct tta atg aat aat ttc cgt caa tat   2657
Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr
        190                 195                 200
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tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct ttt gtc ttt ggc   2705
Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly
    205                 210                 215

gct ggt aaa cca tat gaa ttt tct att gat tgt gac aaa ata aac tta   2753
Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu
220                 225                 230                 235

ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc acc ttt atg tat   2801
Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr
                240                 245                 250

gta ttt tct acg ttt gct aac ata ctg cgt aat aag gag tct taatc atg 2851
Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser      Met
            255                 260                 265

cca gtt ctt ttg ggt att ccg tta tta ttg cgt ttc ctc ggt           2893
Pro Val Leu Leu Gly Ile Pro Leu Leu Leu Arg Phe Leu Gly
            270                 275                 280

ttccttctgg taactttgtt cggctatctg cttacttttc ttaaaaaggg cttcggtaag 2953

atagctattg ctatttcatt gtttcttgct cttattattg ggcttaactc aattcttgtg 3013

ggttatctct ctgatattag cgctcaatta ccctctgact ttgttcaggg tgttcagtta 3073

attctcccgt ctaatgcgct tccctgtttt tatgttattc tctctgtaaa ggctgctatt 3133

ttcatttttg acgttaaaca aaaaatcgtt tcttatttgg attgggataa ataat atg  3191
                                                            Met

gct gtt tat ttt gta act ggc aaa tta ggc tct gga aag acg ctc gtt   3239
Ala Val Tyr Phe Val Thr Gly Lys Leu Gly Ser Gly Lys Thr Leu Val
            285                 290                 295

agc gtt ggt aag att cag gat aaa att gta gct ggg tgc aaa ata gca   3287
Ser Val Gly Lys Ile Gln Asp Lys Ile Val Ala Gly Cys Lys Ile Ala
        300                 305                 310

act aat ctt gat tta agg ctt caa aac ctc ccg caa gtc ggg agg ttc   3335
Thr Asn Leu Asp Leu Arg Leu Gln Asn Leu Pro Gln Val Gly Arg Phe
    315                 320                 325

gct aaa acg cct cgc gtt ctt aga ata ccg gat aag cct tct ata tct   3383
Ala Lys Thr Pro Arg Val Leu Arg Ile Pro Asp Lys Pro Ser Ile Ser
330                 335                 340                 345

gat ttg ctt gct att ggg cgc ggt aat gat tcc tac gat gaa aat aaa   3431
Asp Leu Leu Ala Ile Gly Arg Gly Asn Asp Ser Tyr Asp Glu Asn Lys
                350                 355                 360

aac ggc ttg ctt gtt ctc gat gag tgc ggt act tgg ttt aat acc cgt   3479
Asn Gly Leu Leu Val Leu Asp Glu Cys Gly Thr Trp Phe Asn Thr Arg
            365                 370                 375

tct tgg aat gat aag gaa aga cag ccg att att gat tgg ttt cta cat   3527
Ser Trp Asn Asp Lys Glu Arg Gln Pro Ile Ile Asp Trp Phe Leu His
        380                 385                 390
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gct cgt aaa tta gga tgg gat att att ttt ctt gtt cag gac tta tct   3575
Ala Arg Lys Leu Gly Trp Asp Ile Ile Phe Leu Val Gln Asp Leu Ser
    395                 400                 405

att gtt gat aaa cag gcg cgt tct gca tta gct gaa cat gtt gtt tat   3623
Ile Val Asp Lys Gln Ala Arg Ser Ala Leu Ala Glu His Val Val Tyr
410                 415                 420                 425

tgt cgt cgt ctg gac aga att act tta cct ttt gtc ggt act tta tat   3671
Cys Arg Arg Leu Asp Arg Ile Thr Leu Pro Phe Val Gly Thr Leu Tyr
                430                 435                 440

tct ctt att act ggc tcg aaa atg cct ctg cct aaa tta cat gtt ggc   3719
Ser Leu Ile Thr Gly Ser Lys Met Pro Leu Pro Lys Leu His Val Gly
            445                 450                 455

gtt gtt aaa tat ggc gat tct caa tta agc cct act gtt gag cgt tgg   3767
Val Val Lys Tyr Gly Asp Ser Gln Leu Ser Pro Thr Val Glu Arg Trp
        460                 465                 470

ctt tat act ggt aag aat ttg tat aac gca tat gat act aaa cag gct   3815
Leu Tyr Thr Gly Lys Asn Leu Tyr Asn Ala Tyr Asp Thr Lys Gln Ala
    475                 480                 485

ttt tct agt aat tat gat tcc ggt gtt tat tct tat tta acg cct tat   3863
Phe Ser Ser Asn Tyr Asp Ser Gly Val Tyr Ser Tyr Leu Thr Pro Tyr
490                 495                 500                 505

tta tca cac ggt cgg tat ttc aaa cca tta aat tta ggt cag aag atg   3911
Leu Ser His Gly Arg Tyr Phe Lys Pro Leu Asn Leu Gly Gln Lys Met
                510                 515                 520

aaa tta act aaa ata tat ttg aaa aag ttt tct cgc gtt ctt tgt ctt   3959
Lys Leu Thr Lys Ile Tyr Leu Lys Lys Phe Ser Arg Val Leu Cys Leu
            525                 530                 535

gcg att gga ttt gca tca gca ttt aca tat agt tat ata acc caa cct   4007
Ala Ile Gly Phe Ala Ser Ala Phe Thr Tyr Ser Tyr Ile Thr Gln Pro
        540                 545                 550

aag ccg gag gtt aaa aag gta gtc tct cag acc tat gat ttt gat aaa   4055
Lys Pro Glu Val Lys Lys Val Val Ser Gln Thr Tyr Asp Phe Asp Lys
    555                 560                 565

ttc act att gac tct tct cag cgt ctt aat cta agc tat cgc tat gtt   4103
Phe Thr Ile Asp Ser Ser Gln Arg Leu Asn Leu Ser Tyr Arg Tyr Val
570                 575                 580                 585

ttc aag gat tct aag gga aaa tta att aat agc gac gat tta cag aag   4151
Phe Lys Asp Ser Lys Gly Lys Leu Ile Asn Ser Asp Asp Leu Gln Lys
                590                 595                 600

caa ggt tat tca ctc aca tat att gat tta tgt act gtt tcc att aaa   4199
Gln Gly Tyr Ser Leu Thr Tyr Ile Asp Leu Cys Thr Val Ser Ile Lys
            605                 610                 615

aaa ggt aat tca aat gaa att gtt aaa tgt aat taattttgtt ttcttgatgt 4252
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Lys Gly Asn Ser Asn Glu Ile Val Lys Cys Asn
620 625

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ttgtaacttg gtattcaaag caatcaggcg aatccgttat tgtttctccc gatgtaaaag 4372

gtactgttac tgtatattca tctgacgtta aacctgaaaa tctacgcaat ttctttattt 4432

ctgttttacg tgcaaataat tttgatatgg taggttctaa cccttccatt attcagaagt 4492

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atgataattc cgctccttct ggtggtttct ttgttccgca aaatgataat gttactcaaa 4612

cttttaaaat taataacgtt cgggcaaagg atttaatacg agttgtcgaa ttgtttgtaa 4672

agtctaatac ttctaaatcc tcaaatgtat tatctattga cggctctaat ctattagttg 4732

ttagtgctcc taaagatatt ttagataacc ttcctcaatt cctttcaact gttgatttgc 4792

caactgacca gatattgatt gagggtttga tatttgaggt tcagcaaggt gatgctttag 4852

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gatttgggtg atggttcacg tagtgggcca tcgccctgat agacggtttt tcgccctttg 5752

acgttggagt ccacgttctt taatagtgga ctcttgttcc aaactggaac aacactcaac 5812

cctatctcgg gctattcttt tgatttataa gggattttgc cgatttcgga accaccatca 5872

aacaggattt tcgcctgctg gggcaaacca gcgtggaccg cttgctgcaa ctctctcagg 5932

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gccaggcggt gaagggcaat cagctgttgc ccgtctcact ggtgaaaaga aaaaccaccc 5992

tggatccaag cttgcaggtg gcacttttcg gggaaatgtg cgcggaaccc ctatttgttt 6052

atttttctaa atacattcaa atatgtatcc gctcatgaga caataaccct gataaatgct 6112

tcaataatat tgaaaaagga agagtatgag tattcaacat ttccgtgtcg cccttattcc 6172

ctttttgcg gcattttgcc ttcctgtttt tgctcaccca gaaacgctgg tgaaagtaaa 6232

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tctgctatgt ggcgcggtat tatcccgtat tgacgccggg caagagcaac tcggtcgccg 6412

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tacgtaagac ccccaagctt gtcgactgaa tggcgaatgg cgctttgcct ggtttccggc 7192

accagaagcg gtgccggaaa gctggctgga gtgcgatctt cctgacgctc gagcgcaacg 7252

caattaatgt gagttagctc actcattagg caccccaggc tttacacttt atgcttccgg 7312

ctcgtatgtt gtgtggaatt gtgagcggat aacaatttca cacaggaaac agctatgacc 7372

atgattacgc caagctttgg agccttttt ttggagattt tcaac gtg aaa aaa tta 7429
                                                Met Lys Lys Leu
                                                     630

tta ttc gca att cct tta gtt gtt cct ttc tat tct cac agt gca caa   7477
Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser His Ser Ala Gln
        635                 640                 645

gac atc cag atg acc cag tct cca gcc acc ctg tct ttg tct cca ggg   7525
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Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
    650                 655                 660

gaa aga gcc acc ctc tcc tgc agg gcc agt cag ggt gtt agc agc tac   7573
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly Val Ser Ser Tyr
665                 670                 675                 680

tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc atc   7621
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
                685                 690                 695

tat gat gca tcc aac agg gcc act ggc atc cca gcc agg ttc agt ggc   7669
Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
            700                 705                 710

agt ggg cct ggg aca gac ttc act ctc acc atc agc agc cta gag cct   7717
Ser Gly Pro Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
        715                 720                 725

gaa gat ttt gca gtt tat tac tgt cag cag cgt aac tgg cat ccg tgg   7765
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Asn Trp His Pro Trp
    730                 735                 740

acg ttc ggc caa ggg acc aag gtg gaa atc aaa cga act gtg gct gca   7813
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
745                 750                 755                 760

cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct gga   7861
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
                765                 770                 775

act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag gcc   7909
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
            780                 785                 790

aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc cag   7957
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
        795                 800                 805

gag agt gtc aca gag cgg gac agc aag gac agc acc tac agc ctc agc   8005
Glu Ser Val Thr Glu Arg Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
    810                 815                 820

agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc tac   8053
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
825                 830                 835                 840

gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag agc   8101
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
                845                 850                 855

ttc aac agg gga gag tgt taataaggcg cgccaattct atttcaagga          8149
Phe Asn Arg Gly Glu Cys
            860

gacagtcata atg aaa tac cta ttg cct acg gca gcc gct gga ttg tta     8198
          Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu
                865                 870                 875
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tta ctc gcg gcc cag ccg gcc atg gcc gaa gtt caa ttg tta gag tct   8246
Leu Leu Ala Ala Gln Pro Ala Met Ala Glu Val Gln Leu Leu Glu Ser
                880                 885                 890

ggt ggc ggt ctt gtt cag cct ggt ggt tct tta cgt ctt tct tgc gct   8294
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
            895                 900                 905

gct tcc gga ttc act ttc tct act tac gag atg cgt tgg gtt cgc caa   8342
Ala Ser Gly Phe Thr Phe Ser Thr Tyr Glu Met Arg Trp Val Arg Gln
        910                 915                 920

gct cct ggt aaa ggt ttg gag tgg gtt tct tat atc gct cct tct ggt   8390
Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ala Pro Ser Gly
    925                 930                 935

ggc gat act gct tat gct gac tcc gtt aaa ggt cgc ttc act atc tct   8438
Gly Asp Thr Ala Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
940                 945                 950                 955

aga gac aac tct aag aat act ctc tac ttg cag atg aac agc tta agg   8486
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
                960                 965                 970

gct gag gac act gca gtc tac tat tgt gcg agg agg ctc gat ggc tat   8534
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Arg Leu Asp Gly Tyr
            975                 980                 985

att tcc tac tac tac ggt atg gac gtc tgg ggc caa ggg acc acg gtc   8582
Ile Ser Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
        990                 995                1000

acc gtc tca agc gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca   8630
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
   1005                1010                1015

ccc tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg   8678
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
1020                1025                1030                1035

gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc   8726
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
                1040                1045                1050

gcc ctg acc agc ggc gtc cac acc ttc ccg gct gtc cta cag tcc tca   8774
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
            1055                1060                1065

gga ctc tac tcc ctc agc agc gta gtg acc gtg ccc tcc agc agc ttg   8822
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
        1070                1075                1080

ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc   8870
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
   1085                1090                1095

aag gtg gac aag aaa gtt gag ccc aaa tct tgt gcg gcc gca cat cat   8918
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Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Ala Ala Ala His His
1100                1105                1110                1115

cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag gat   8966
His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp
                1120                1125                1130

ctg aat ggg gcc gca tag gct agc tct gct wsy ggy gay tty gay tay   9014
Leu Asn Gly Ala Ala Gln Ala Ser Ser Ala Ser Gly Asp Phe Asp Tyr
            1135                1140                1145

gar aar atg gct aaw gcy aay aar ggs gcy atg acy gar aay gcy gay   9062
Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp
        1150                1155                1160

gar aay gck ytr car wsy gay gcy aar ggy aar ytw gay wsy gtc gck   9110
Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala
    1165                1170                1175

acy gay tay ggy gcy gcc atc gay ggy tty aty ggy gay gtc wsy ggy   9158
Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly
1180                1185                1190                1195

ytk gcy aay ggy aay ggy gcy acy ggw gay tty gcw ggy tck aat tcy   9206
Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser
                1200                1205                1210

car atg gcy car gty ggw gay ggk gay aay wsw cck ytw atg aay aay   9254
Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn
            1215                1220                1225

tty mgw car tay ytw cck tcy cty cck car wsk gty gar tgy cgy ccw   9302
Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro
        1230                1235                1240

tty gty tty wsy gcy ggy aar ccw tay gar tty wsy aty gay tgy gay   9350
Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp
    1245                1250                1255

aar atm aay ytw tty cgy ggy gty tty gck tty ytk yta tay gty gcy   9398
Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala
1260                1265                1270                1275

acy tty atg tay gtw tty wsy ack tty gcy aay atw ytr cgy aay aar   9446
Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys
                1280                1285                1290

gar wsy tagtgatctc ctaggaagcc cgcctaatga gcgggctttt tttttctggt   9502
Glu Ser

atgcatcctg aggccgatac tgtcgtcgtc ccctcaaact ggcagatgca cggttacgat 9562

gcgcccatct acaccaacgt gacctatccc attacggtca atccgccgtt tgttcccacg 9622

gagaatccga cgggttgtta ctcgctcaca tttaatgttg atgaaagctg gctacaggaa 9682

ggccagacgc gaattatttt tgatggcgtt cctattggtt aaaaaatgag ctgatttaac 9742
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tagttttacg attaccgttc atcgattctc ttgtttgctc cagactctca ggcaatgacc 9922

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tgccttgcct gtatgattta ttggatgtt 10251

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<211> 113
<212> PRT
<213> Artificial Sequence

<220>
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protein sequence

<400> 583
Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
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Gly Ala Ala Glu Ser His Leu Asp Gly Ala Ala Glu Thr Val Glu Ser
20 25 30

Cys Leu Ala Lys Ser His Thr Glu Asn Ser Phe Thr Asn Val Trp Lys
35 40 45

Asp Asp Lys Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp
50 55 60

Asn Ala Thr Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr
65 70 75 80

Gly Thr Trp Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu Gly Gly
85 90 95

Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
100 105 110

Thr

<210> 584
<211> 152
<212> PRT
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protein sequence

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Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala
1 5 10 15

Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly
20 25 30

Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe
35 40 45

Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp
50 55 60

Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn
65 70 75 80

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
85 90 95

Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu
100 105 110

Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala
115 120 125

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala
130 135 140

Asn Ile Leu Arg Asn Lys Glu Ser
145 150

<210> 585
<211> 15
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peptide sequence

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1 5 10 15

<210> 586
<211> 348
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protein sequence

<400> 586

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Met Ala Val Tyr Phe Val Thr Gly Lys Leu Gly Ser Gly Lys Thr Leu
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Val Ser Val Gly Lys Ile Gln Asp Lys Ile Val Ala Gly Cys Lys Ile
            20                  25                  30

Ala Thr Asn Leu Asp Leu Arg Leu Gln Asn Leu Pro Gln Val Gly Arg
        35                  40                  45

Phe Ala Lys Thr Pro Arg Val Leu Arg Ile Pro Asp Lys Pro Ser Ile
    50                  55                  60

Ser Asp Leu Leu Ala Ile Gly Arg Gly Asn Asp Ser Tyr Asp Glu Asn
65                  70                  75                  80

Lys Asn Gly Leu Leu Val Leu Asp Glu Cys Gly Thr Trp Phe Asn Thr
                85                  90                  95

Arg Ser Trp Asn Asp Lys Glu Arg Gln Pro Ile Ile Asp Trp Phe Leu
            100                 105                 110

His Ala Arg Lys Leu Gly Trp Asp Ile Ile Phe Leu Val Gln Asp Leu
        115                 120                 125

Ser Ile Val Asp Lys Gln Ala Arg Ser Ala Leu Ala Glu His Val Val
    130                 135                 140

Tyr Cys Arg Arg Leu Asp Arg Ile Thr Leu Pro Phe Val Gly Thr Leu
145                 150                 155                 160

Tyr Ser Leu Ile Thr Gly Ser Lys Met Pro Leu Pro Lys Leu His Val
                165                 170                 175

Gly Val Val Lys Tyr Gly Asp Ser Gln Leu Ser Pro Thr Val Glu Arg
            180                 185                 190

Trp Leu Tyr Thr Gly Lys Asn Leu Tyr Asn Ala Tyr Asp Thr Lys Gln
        195                 200                 205

Ala Phe Ser Ser Asn Tyr Asp Ser Gly Val Tyr Ser Tyr Leu Thr Pro
    210                 215                 220

Tyr Leu Ser His Gly Arg Tyr Phe Lys Pro Leu Asn Leu Gly Gln Lys
225                 230                 235                 240

Met Lys Leu Thr Lys Ile Tyr Leu Lys Lys Phe Ser Arg Val Leu Cys
                245                 250                 255

Leu Ala Ile Gly Phe Ala Ser Ala Phe Thr Tyr Ser Tyr Ile Thr Gln
            260                 265                 270

Pro Lys Pro Glu Val Lys Lys Val Val Ser Gln Thr Tyr Asp Phe Asp
        275                 280                 285

Lys Phe Thr Ile Asp Ser Ser Gln Arg Leu Asn Leu Ser Tyr Arg Tyr
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290 295 300

Val Phe Lys Asp Ser Lys Gly Lys Leu Ile Asn Ser Asp Asp Leu Gln
305 310 315 320

Lys Gln Gly Tyr Ser Leu Thr Tyr Ile Asp Leu Cys Thr Val Ser Ile
325 330 335

Lys Lys Gly Asn Ser Asn Glu Ile Val Lys Cys Asn
340 345

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<213> Artificial Sequence

<220>
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1 5 10 15

His Ser Ala Gln Asp Ile Gln Met Thr Gln Ser Pro Ala Thr Leu Ser
20 25 30

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Gly
35 40 45

Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
50 55 60

Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala
65 70 75 80

Arg Phe Ser Gly Ser Gly Pro Gly Thr Asp Phe Thr Leu Thr Ile Ser
85 90 95

Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Asn
100 105 110

Trp His Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
115 120 125

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
130 135 140

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
145 150 155 160

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
165 170 175

Gly Asn Ser Gln Glu Ser Val Thr Glu Arg Asp Ser Lys Asp Ser Thr
180 185 190

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
195 200 205

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
210 215 220

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230

<210> 588
<211> 431
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CJRA05 protein sequence

<400> 588
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Leu Glu Ser Gly Gly Gly
20 25 30

Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Thr Tyr Glu Met Arg Trp Val Arg Gln Ala Pro Gly
50 55 60

Lys Gly Leu Glu Trp Val Ser Tyr Ile Ala Pro Ser Gly Gly Asp Thr
65 70 75 80

Ala Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Arg Leu Asp Gly Tyr Ile Ser Tyr
115 120 125

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
130 135 140

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
145 150 155 160

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
165 170 175

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
180 185 190

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
195 200 205

```
Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
    210                 215                 220

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
225                 230                 235                 240

Lys Lys Val Glu Pro Lys Ser Cys Ala Ala Ala His His His His His
                245                 250                 255

His Gly Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly
            260                 265                 270

Ala Ala Gln Ala Ser Ser Ala Ser Gly Asp Phe Asp Tyr Glu Lys Met
        275                 280                 285

Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala
    290                 295                 300

Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr
305                 310                 315                 320

Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn
                325                 330                 335

Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala
            340                 345                 350

Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln
        355                 360                 365

Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe
    370                 375                 380

Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn
385                 390                 395                 400

Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met
                405                 410                 415

Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
            420                 425                 430
```

<210> 589
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative peptide

<400> 589

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Glu Gly Gly Gly Ser
  1               5
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<210> 590
<211> 1275
<212> DNA
<213> Unknown Organism

<220>
<221> CDS
<222> (1)..(1272)

<220>
<223> Description of Unknown Organism: M13 nucleotide sequence

<400> 590

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gtg aaa aaa tta tta ttc gca att cct tta gtt gtt cct ttc tat tct   48
Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
  1               5                  10                  15

cac tcc gct gaa act gtt gaa agt tgt tta gca aaa ccc cat aca gaa   96
His Ser Ala Glu Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu
             20                  25                  30

aat tca ttt act aac gtc tgg aaa gac gac aaa act tta gat cgt tac   144
Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr
         35                  40                  45

gct aac tat gag ggt tgt ctg tgg aat gct aca ggc gtt gta gtt tgt   192
Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys
     50                  55                  60

act ggt gac gaa act cag tgt tac ggt aca tgg gtt cct att ggg ctt   240
Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu
 65                  70                  75                  80

gct atc cct gaa aat gag ggt ggt ggc tct gag ggt ggc ggt tct gag   288
Ala Ile Pro Glu Asn Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
                 85                  90                  95

ggt ggc ggt tct gag ggt ggc ggt act aaa cct cct gag tac ggt gat   336
Gly Gly Gly Ser Glu Gly Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp
            100                 105                 110

aca cct att ccg ggc tat act tat atc aac cct ctc gac ggc act tat   384
Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr
        115                 120                 125

ccg cct ggt act gag caa aac ccc gct aat cct aat cct tct ctt gag   432
Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu
    130                 135                 140

gag tct cag cct ctt aat act ttc atg ttt cag aat aat agg ttc cga   480
Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg
145                 150                 155                 160

aat agg cag ggg gca tta act gtt tat acg ggc act gtt act caa ggc   528
Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly
                165                 170                 175
```

```
act gac ccc gtt aaa act tat tac cag tac act cct gta tca tca aaa   576
Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys
            180                 185                 190

gcc atg tat gac gct tac tgg aac ggt aaa ttc aga gac tgc gct ttc   624
Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe
        195                 200                 205

cat tct ggc ttt aat gag gat cca ttc gtt tgt gaa tat caa ggc caa   672
His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln
    210                 215                 220

tcg tct gac ctg cct caa cct cct gtc aat gct ggc ggc ggc tct ggt   720
Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly
225                 230                 235                 240

ggt ggt tct ggt ggc ggc tct gag ggt ggt ggc tct gag ggt ggc ggt   768
Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
                245                 250                 255

tct gag ggt ggc ggc tct gag gga ggc ggt tcc ggt ggt ggc tct ggt   816
Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly
            260                 265                 270

tcc ggt gat ttt gat tat gaa aag atg gca aac gct aat aag ggg gct   864
Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala
        275                 280                 285

atg acc gaa aat gcc gat gaa aac gcg cta cag tct gac gct aaa ggc   912
Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly
    290                 295                 300

aaa ctt gat tct gtc gct act gat tac ggt gct gct atc gat ggt ttc   960
Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe
305                 310                 315                 320

att ggt gac gtt tcc ggc ctt gct aat ggt aat ggt gct act ggt gat  1008
Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp
                325                 330                 335

ttt gct ggc tct aat tcc caa atg gct caa gtc ggt gac ggt gat aat  1056
Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn
            340                 345                 350

tca cct tta atg aat aat ttc cgt caa tat tta cct tcc ctc cct caa  1104
Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
        355                 360                 365

tcg gtt gaa tgt cgc cct ttt gtc ttt agc gct ggt aaa cca tat gaa  1152
Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu
    370                 375                 380

ttt tct att gat tgt gac aaa ata aac tta ttc cgt ggt gtc ttt gcg  1200
Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala
385                 390                 395                 400

ttt ctt tta tat gtt gcc acc ttt atg tat gta ttt tct acg ttt gct  1248
Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala
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405 410 415

aac ata ctg cgt aat aag gag tct taa 1275
Asn Ile Leu Arg Asn Lys Glu Ser
420

<210> 591
<211> 424
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: M13 protein sequence

<400> 591
Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ser
1 5 10 15

His Ser Ala Glu Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu
20 25 30

Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr Leu Asp Arg Tyr
35 40 45

Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly Val Val Val Cys
50 55 60

Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val Pro Ile Gly Leu
65 70 75 80

Ala Ile Pro Glu Asn Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu
85 90 95

Gly Gly Gly Ser Glu Gly Gly Gly Thr Lys Pro Pro Glu Tyr Gly Asp
100 105 110

Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr
115 120 125

Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu
130 135 140

Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg
145 150 155 160

Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly
165 170 175

Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys
180 185 190

Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe
195 200 205

His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln
210 215 220

```
Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly Gly Gly Ser Gly
225                 230                 235                 240

Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly
                245                 250                 255

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly
            260                 265                 270

Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala
        275                 280                 285

Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly
    290                 295                 300

Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe
305                 310                 315                 320

Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp
                325                 330                 335

Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn
            340                 345                 350

Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln
        355                 360                 365

Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu
    370                 375                 380

Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala
385                 390                 395                 400

Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala
                405                 410                 415

Asn Ile Leu Arg Asn Lys Glu Ser
            420
```

<210> 592
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 592
caacgatgat cgtatggcgc atgctgccga gacag 35

<210> 593
<211> 1355
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: M13-III nucleotide sequence

<220>
<221> CDS
<222> (1)..(1305)

<400> 593

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gcg gcc gca cat cat cat cac cat cac ggg gcc gca gaa caa aaa ctc   48
Ala Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu
  1               5                  10                  15

atc tca gaa gag gat ctg aat ggg gcc gca tag gct agc gat atc aac   96
Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala     Ala Ser Asp Ile Asn
             20                  25                  30

gat gat cgt atg gct tct act gcy gar acw gty gaa wsy tgy ytr gcm   144
Asp Asp Arg Met Ala Ser Thr Ala Glu Thr Val Glu Ser Cys Leu Ala
             35                  40                  45

aar ccy cay acw gar aat wsw tty acw aay gts tgg aar gay gay aar   192
Lys Pro His Thr Glu Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys
         50                  55                  60

acy ytw gat cgw tay gcy aay tay gar ggy tgy ytr tgg aat gcy acm   240
Thr Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr
     65                  70                  75

ggc gty gtw gty tgy ack ggy gay gar acw car tgy tay ggy acr tgg   288
Gly Val Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp
 80                  85                  90                  95

gtk cck atw ggs ytw gcy atm cck gar aay gar ggy ggy ggy wsy gar   336
Val Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu Gly Gly Gly Ser Glu
                100                 105                 110

ggy ggy ggy wsy gar ggy ggy ggw tcy gar ggw ggy ggw acy aar cck   384
Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Thr Lys Pro
            115                 120                 125

cck gar tay ggy gay acw cck atw cck ggy tay acy tay aty aay cck   432
Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro
        130                 135                 140

ytm gay ggm acy tay cck cck ggy acy gar car aay ccy gcy aay cck   480
Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro
    145                 150                 155

aay ccw wsy ytw gar gar wsy car cck ytw aay acy tty atg tty car   528
Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln
160                 165                 170                 175

aay aay mgk tty mgr aay mgk car ggk gcw ytw acy gtk tay ack ggm   576
Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly
                180                 185                 190
```

```
acy gty acy car ggy acy gay ccy gty aar acy tay tay car tay acy   624
Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr
            195                 200                 205

cck gtm tcr wsw aar gcy atg tay gay gcy tay tgg aay ggy aar tty   672
Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe
        210                 215                 220

mgw gay tgy gcy tty cay wsy ggy tty aay gar gay ccw tty gty tgy   720
Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys
    225                 230                 235

gar tay car ggy car wsk wsy gay ytr cck car ccw cck gty aay gck   768
Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala
240                 245                 250                 255

ggy ggy ggy wsy ggy ggw ggy wsy ggy ggy ggy wsy gar ggy ggw ggy   816
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly
                260                 265                 270

wsy gar ggw ggy ggy wsy ggr ggy ggy wsy ggy wsy ggy gay tty gay   864
Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp
            275                 280                 285

tay gar aar atg gcw aay gcy aay aar ggs gcy atg acy gar aay gcy   912
Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala
        290                 295                 300

gay gar aay gcr ctr car wst gay gcy aar ggy aar ytw gay wsy gtc   960
Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val
    305                 310                 315

gcy acw gay tay ggt gct gcy atc gay ggy tty aty ggy gay gty wsy   1008
Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser
320                 325                 330                 335

ggy ctk gct aay ggy aay ggw gcy acy ggw gay tty gcw ggy tck aat   1056
Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn
                340                 345                 350

tcy car atg gcy car gty ggw gay ggk gay aay wsw cck ytw atg aay   1104
Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn
            355                 360                 365

aay tty mgw car tay ytw cck tcy cty cck car wsk gty gar tgy cgy   1152
Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg
        370                 375                 380

ccw tty gty tty wsy gcy ggy aar ccw tay gar tty wsy aty gay tgy   1200
Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys
    385                 390                 395

gay aar atm aay ytw ttc cgy ggy gty tty gck tty ytk yta tay gty   1248
Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val
400                 405                 410                 415

gcy acy tty atg tay gtw tty wsy ack tty gcy aay atw ytr cgy aay   1296
Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn
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420 425 430

aar gar wsy tagtgatctc ctaggaagcc cgcctaatga gcgggctttt 1345
Lys Glu Ser

tttttctggt 1355

<210> 594
<211> 434
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: M13-III protein sequence

<400> 594
Ala Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu
1 5 10 15

Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala Ala Ser Asp Ile Asn Asp
20 25 30

Asp Arg Met Ala Ser Thr Ala Glu Thr Val Glu Ser Cys Leu Ala Lys
35 40 45

Pro His Thr Glu Asn Ser Phe Thr Asn Val Trp Lys Asp Asp Lys Thr
50 55 60

Leu Asp Arg Tyr Ala Asn Tyr Glu Gly Cys Leu Trp Asn Ala Thr Gly
65 70 75 80

Val Val Val Cys Thr Gly Asp Glu Thr Gln Cys Tyr Gly Thr Trp Val
85 90 95

Pro Ile Gly Leu Ala Ile Pro Glu Asn Glu Gly Gly Gly Ser Glu Gly
100 105 110

Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Thr Lys Pro Pro
115 120 125

Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr Ile Asn Pro Leu
130 135 140

Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro Ala Asn Pro Asn
145 150 155 160

Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe Met Phe Gln Asn
165 170 175

Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val Tyr Thr Gly Thr
180 185 190

Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr Gln Tyr Thr Pro
195 200 205

Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn Gly Lys Phe Arg
210 215 220

Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro Phe Val Cys Glu
225 230 235 240

Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro Val Asn Ala Gly
245 250 255

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser
260 265 270

Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr
275 280 285

Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp
290 295 300

Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala
305 310 315 320

Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly
325 330 335

Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser
340 345 350

Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn
355 360 365

Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro
370 375 380

Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp
385 390 395 400

Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala
405 410 415

Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys
420 425 430

Glu Ser

<210> 595
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 595
cgttgatatc gctagcctat gc 22

<210> 596
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 596
gataggctta gctagcccgg agaacgaagg 30

<210> 597
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 597
ctttcacagc ggtttcgcta gcgacccttt tgtctgc 37

<210> 598
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 598
ctttcacagc ggtttcgcta gcgacccttt tgtcagcgag taccagggtc 50

<210> 599
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 599
gactgtctcg gcagcatgcg ccatacgatc atcgttg 37

<210> 600
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> CDS
<222> (2)..(25)

<400> 600
c aac gat gat cgt atg gcg cat gct gccgagacag tc 37
Asn Asp Asp Arg Met Ala His Ala
1 5

<210> 601
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 601
Asn Asp Asp Arg Met Ala His Ala
1 5

<210> 602
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 602
ctttcacagc ggtttgcatg cagacccttt tgtctgc 37

<210> 603
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 603
ctttcacagc ggtttgcatg cagacccttt tgtcagcgag taccagggtc 50

<210> 604
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative peptide

<400> 604
Tyr Ala Asp Ser Val Lys Gly
1 5

<210> 605
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 605
cctcgacagc gaagtgcaca g 21

<210> 606
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 606
ggctgagtca agacgctctg tgcacttcgc tgtcgagg 38

<210> 607
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative peptide

<400> 607
Gln Ser Ala Leu Thr Gln Pro
1 5

<210> 608
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 608
cctctgtcac agtgcacaag ac 22

<210> 609
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 609
cctctgtcac agtgcacaag acatccagat gacccagtct cc 42

<210> 610
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 610
gggaggatgg agactgggtc gtctggatgt cttgtgcact gtgacagagg 50

<210> 611
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative peptide

<400> 611
Gln Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
1 5 10

<210> 612
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 612
gactgggtgt agtgatctag 20

<210> 613
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 613
ggtgtagtga tcttctagtg acaactct 28

<210> 614
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 614
Val Ser Ser Arg Asp Asn
1 5

<210> 615
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> CDS
<222> (1)..(15)

<400> 615
tac tat tgt gcg aaa 15
Tyr Tyr Cys Ala Lys
1 5

<210> 616
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 616
Tyr Tyr Cys Ala Lys
1 5

<210> 617
<211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 617
ggtgccgata ggcttgcatg caccggagaa cgaagg 36

<210> 618
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 618
cgcttcacta agtctagaga caactctaag aatactctct acttgcagat gaacagctta 60
agggctgagg acactgcagt ctactattgt acgag 95

<210> 619
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (4)..(7)
<223> A, T, C, G, other or unknown

<400> 619
gatnnnnatc 10

<210> 620
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: MALIA3-derived
peptide

<400> 620
Met Lys Leu Leu Asn Val Ile Asn Phe Val
1 5 10

<210> 621

<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CJRA05-derived peptide

<400> 621
Met Ser Val Leu Val Tyr Ser Phe Ala Ser Phe Val Leu Gly Trp Cys
1 5 10 15

Leu Arg Ser Gly Ile Thr Tyr Phe Thr Arg Leu Met Glu
20 25

<210> 622
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative nucleotide sequence

<400> 622
ttttttttt ttttt 15

<210> 623
<211> 87
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: MALIA3-derived peptide

<400> 623
Met Ile Lys Val Glu Ile Lys Pro Ser Gln Ala Gln Phe Thr Thr Arg
1 5 10 15

Ser Gly Val Ser Arg Gln Gly Lys Pro Tyr Ser Leu Asn Glu Gln Leu
20 25 30

Cys Tyr Val Asp Leu Gly Asn Glu Tyr Pro Val Leu Val Lys Ile Thr
35 40 45

Leu Asp Glu Gly Gln Pro Ala Tyr Ala Pro Gly Leu Tyr Thr Val His
50 55 60

Leu Ser Ser Phe Lys Val Gly Gln Phe Gly Ser Leu Met Ile Asp Arg
65 70 75 80

Leu Arg Leu Val Pro Ala Lys
85

<210> 624
<211> 29
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: MALIA3-derived peptide

<400> 624
Met Ser Val Leu Val Tyr Ser Phe Ala Ser Phe Val Leu Gly Trp Cys
1 5 10 15

Leu Arg Ser Gly Ile Thr Tyr Phe Thr Arg Leu Met Glu
20 25

<210> 625
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<220>
<221> modified_base
<222> (7)..(10)
<223> A, T, C, G, other or unknown

<400> 625
ctcttcnnnn 10

<210> 626
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CJRA05-derived peptide

<400> 626
Met Ile Lys Val Glu Ile Lys Pro Ser Gln Ala Gln Phe Thr Thr Arg
1 5 10 15

Ser Gly Val Ser Arg Gln Gly Lys Pro Tyr Ser Leu Asn Glu Gln Leu
20 25 30

Cys Tyr Val Asp Leu Gly Asn Glu Tyr Pro Val Leu Val Lys Ile Thr
35 40 45

Leu Asp Glu Gly Gln Pro Ala Tyr Ala Pro Gly Leu Tyr Thr Val His
50 55 60

Leu Ser Ser Phe Lys Val Gly Gln Phe Gly Ser Leu Met Ile Asp Arg

65 70 75 80

Leu Arg Leu Val Pro Ala Lys
85

<210> 627
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CJRA05-derived peptide

<400> 627
Met Lys Leu Leu Asn Val Ile Asn Phe Val
1 5 10

<210> 628
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 628
gacccagtct ccatcctcc 19

<210> 629
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 629
gactcagtct ccactctcc 19

<210> 630
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 630
gacgcagtct ccaggcacc 19

<210> 631
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 631
gacgcagtct ccagccacc 19

<210> 632
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 632
gtctcctgga cagtcgatc 19

<210> 633
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 633
ggccttggga cagacagtc 19

<210> 634
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 634
gtctcctgga cagtcagtc 19

<210> 635
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 635
ggccccaggg cagagggtc 19